

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 02:13:54 ; Search time 1520.27 Seconds
(without alignments)
3592.268 Million cell updates/sec

Title: US-10-005-429-14

Perfect score: 652

Sequence: 1 MAABEGAVIACHTKDFDAR.....DAVRKYAAAGTTTAPASASA 126

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:

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16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
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26: em.ro:*
27: em.scs:*
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39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	361	55.4	526	11	G73679 RZ498R etio
2	361	55.4	600	8	AK059196 Oryza sat
3	361	55.4	601	8	OSU92541 U2541 Oryza sativ
4	361	55.4	686	6	E08194 RPS13 Gene
5	361	55.4	687	8	D21836 Oryza sativ
6	361	55.4	733	8	AK121423 Oryza sat
7	338	51.8	357	8	AY245454 Hordeum v
8	333	51.1	598	8	AY072771 Triticum
9	315	48.3	466	6	AB414207 Sequence
10	315	48.3	466	6	BD109760 EST and e
11	305.5	47.0	590	6	AY088698 Arabidops
12	305.5	46.9	360	6	AX505469 Sequence
13	305.5	46.9	360	8	BT004710 Arabidops
14	305.5	46.9	556	8	AK118542 Arabidops
15	301.5	46.2	642	8	Z35473 A.thaliana
16	285	43.7	564	8	AF332593 Prunus pe
17	284	43.6	345	8	AF43265 Populus t
18	282	43.3	345	6	AX505468 Sequence
19	282	43.3	480	8	AY088687 Arabidops
20	282	43.3	497	8	Z14084 A.thaliana
21	278	42.6	676	8	AY344230 Ipomoea b
22	275.5	42.3	580	8	BNU59380 Brassica na
23	272	41.7	731	8	AY344229 Ipomoea b
24	272	41.7	784	8	AY344229 Citrus x
25	271	41.6	698	8	NTTRNA X8527 N.tabacum m
26	267	41.0	596	8	TAE9762 R.communis
27	262	40.2	596	6	AR016869 Triticum
28	261	40.0	653	6	AR016869 Sequence
29	261	40.0	653	6	AR020895 Sequence
30	261	40.0	653	6	AR027218 Sequence
31	261	40.0	653	6	AR036505 Sequence
32	261	40.0	653	6	AR064647 Sequence
33	261	40.0	653	6	AR067572 Sequence
34	261	40.0	653	6	I38524 Sequence 10
35	261	40.0	653	6	I56939 Sequence 10
36	261	40.0	653	6	I59865 Sequence 10
37	261	40.0	653	6	I75192 Sequence 10
38	261	40.0	653	6	AR403740 Sequence
39	259.5	39.8	595	8	D87994 Paspalum e
40	256.5	39.3	641	8	AF051206 Picea mar
41	254	39.0	366	6	AX654096 Sequence
42	254	39.0	682	8	AK059385 Oryza sat
43	254	39.0	740	8	AB053294 Oryza sat
44	254	39.0	3740	8	AK106758 Oryza sat
45	253	38.8	357	8	AY040028 Arabidops

ALIGNMENTS

RESULT 1

G73679 526 bp DNA linear STS 16-JUL-2002
 RZ488R etiolated leaf tissue of rice Oryza sativa STS genomic clone
 RZ488 sequencing direction=reverse, sequence tagged site.
 G73679
 G73679.1 GI:19697274

STSS
 Oryza sativa (indica cultivar-group)
 Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Erihartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 526)
 McCouch, S.R.
 Oryza sativa STS
 Unpublished (2002)

CONTACT: Susan R. McCouch
 Cornell University
 Dept. of Plant Breeding, Ithaca, NY 14853-1901, USA
 Tel: 6072550420
 Fax: 6072556683
 Email: srm4@cornell.edu
 Primer A: M13 universal Forward GTAAACGACGGCCAGT
 Primer B: M13 Universal Reverse AACAGCTATGACCATG
 STS size: 526
 Protocol:
 Template: 20-100ng
 Primer: 5pmol each
 DNTTPs: 40nmol
 Taq polymerase: 5units
 Total volume: 50ul

Buffer:
 Tris-HCl: 100mM
 KCl: 500mM
 MgCl2: 15mM
 Gelatin: 0.1%
 PH: 8.3

This is a partial sequence of the RFLP clone named above that was
 mapped at Cornell University Plant Breeding Dept. and sequenced at
 the Genome Sequencing Center at Cold Spring Harbor Laboratory. This
 marker is located on rice chromosome 7. For citations and other
 related information concerning this probe, please refer to the
 Gramene database at http:
 Location/Qualifiers
 1..526
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="genomic DNA"
 /cultivar="IR36"
 /db_xref="taxon:39946"
 /map="7"
 /clone="RZ488"
 /clone_lib="etiolated leaf tissue of rice"
 /note="Vector: Lambda ZAP II/pBluescript; V-type: Plasmid;
 A Lambda ZAP II cDNA library was constructed from mRNA
 extracted from etiolated leaf tissue of the rice cultivar
 'IR36' and converted to pBluescript (amp resistant) as
 described in Cause et al. (1994) Genetics 138:1251-1274.
 For insert amplification, use M13 forward and reverse
 primers. Restriction site is EcoRI. Clones from this
 library are designated with the prefix 'RZ'."

STSS
 <1..>526

ORIGIN

Alignment Scores:
 Pred. No.: 7,55e-34 Length: 526
 Score: 361.00 Matches: 70
 Percent Similarity: 71.77% Conservative: 19
 Best Local Similarity: 56.45% Mismatches: 33
 Query Match: 55.37% Indels: 2
 Gaps: 11

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Db	86	ATGGCGCGCCGAGCGAGTGTGATGCGCTGCCACCAACGAGGACGAGTTGCGACGCCGAC	145
Qy	21	MetAlaLysAlaLysGluGlnGlyLysLeuValValLleAspPheMetAlaProTyrCys	40
Db	146	ATGACCAAGCCCAAGGAGCGCCGCAAGTGTGTCTAATTCGCTTCACTGCTTCTCGTGT	205
Qy	41	SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla	60
Db	206	GCCCTTGCCTTCATCGCCCACTGTCGTGATACGCCAAAGTTCCCTGGTGT	265
Qy	61	ValPheLeuGluValAspValAspGluLeuValValAlaLysLleTyrGlyValHis	80
Db	266	GTCCTCTGAGGTTCATGTTGATGAGCTGAAGGAGTGTCTGAAAATACAAATGTCGAG	325
Qy	81	ValMetProThrPheCysPheTleArgAsnGlyGluThrLeuGluSerPheAlaThrVal	100
Db	326	GCAATGCCGACCTTCCTATTCTCAAGATGCTGAGGCTGCACAGGTGCTGGCGGC	385
Qy	101	AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla	120
Db	386	AGGAAGGATGACCTCCAGACACCATCTGTAAGCAC-----GTGGTGGCCACTGCTGCA	439
Qy	121	ProLisSerAla	124
Db	440	TTGCTTCTGCC	451
RESULT	4		
LOCUS	E08194		
DEFINITION	RPS13 gene encoding sieve tube protein.	686 bp	RNA
ACCESSION	E08194		linear
VERSION	E08194.1	GI:2176315	
KEYWORDS	JP 1994269286-A/1.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 686)		
AUTHORS	Kayano,M.		
TITLE	SIEVE TUBE PROTEIN GENE OF PLANT AND METHOD FOR MAKING USEFUL		
JOURNAL	PROTEIN TRANSMIGRATE TO SIEVE TUBE USING THE SAME		
COMMENT	Patent: JP 1994269286-A 1 27-SEP-1994; MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO:KK OS Oryza sativa L., var. aichiasahi PN JP 1994269286-A/1 ED 27-SEP-1994 PF 19-MAR-1993 JP 1993060763 PI KAYANO MITSUO PC C12N15/23,A01H5/00,C12P21/02//C12N5/10; CC strandedness: Double; CC topology: Linear; CC Feature is identified by other; FH Key Location/Qualifiers		
FEATURES			
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FT	/tissue type='leaf'		
FT	/clone='CRSP13-1'		
FT	5'UTR 1..56		
FT	CDS 57..425		
FT	/product='sieve tube protein' FT 3'UTR		
FT	426..686.		
Location/Qualifiers			
1..686			
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/mol_type='genomic RNA'			
/db_xref='taxon:32644'			
ORIGIN			
Alignment Scores:			
Pred. No.:	1..036-33	Length:	686


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/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="J023133N23"

ORIGIN
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Score: 361.00 Matches: 70
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Best Local Similarity: 56.45% Mismatches: 33
Query Match: 55.37% Indels: 2
DB: 8 Gaps: 1

US-10-005-429-14 (1-126) x AK121423 (1-733)
QY 1 MetAlaAGluGluGluValAlaValAlaCysHisThrLysAspGluPheAspAlaAarg 20
Db 95 ATGGCGCGGAGGAGGAGTGTGATCCCTGCCACACAGGAGGAGTTCGAGCCGAC 154
QY 21 MetAlaLysAlaLysGluGluGluValValLysValValLysPheMetAlaProTyrCys 40
Db 155 ATGACCAAGGCCAGGAGCGCGCAAGTGTGATATGACTTCACTGCTTCCTGCTGT 214
QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db 215 GGCCCTTGCCTTCATGCCCGCATGTCGTGATACGCCAAAGATTCCTCGTGTCT 274
QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
Db 275 GTCTCTGAAGTTGATGTTGATGAGCTGAAGGAGTGTGTAAGATCAATGTCGAG 334
QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db 335 GCAATGCGCGACCTTCCTTATTCATCAAGATGCTGAGGCTGACCAAGTCTGTGGCGCC 394
QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaLysIleTyrThrAla 120
Db 395 AGGAGGATGACCTCAGAACACCATCTGTAAGCAC-----GTGCGTGCACCTGCTGCA 448
QY 121 ProAlaSerAla 124
Db 449 TCTGCTTCTGCC 460

RESULT 7
AY245454
LOCUS Hordeum vulgare subsp. vulgare thiorodoxin h isoform 1 mRNA, complete cds.
DEFINITION AY245454.1 GI:32186039
ACCESSION AY245454
VERSION AY245454
KEYWORDS Hordeum
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
REFERENCE Maeda,K., Sminke,C., Ostergaard,O. and Svensson,B.
AUTHORS Identification, cloning and characterization of two thiorodoxin h
TITLE Isoforms, HvTrxh and HvTrxh2, from the barley seed proteome
JOURNAL Eur. J. Biochem. 270 (12), 2633-2643 (2003)
MEDLINE 22671460
PUBMED 12787030
REFERENCE 2 (bases 1 to 357)
AUTHORS Maeda,K., Finnin,C., Ostergaard,O. and Svensson,B.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2003) Chemistry, Carlsberg Laboratory, Gamle
Carlsberg Vej 10, Copenhagen DK-2500 Valby, Denmark
FEATURES
source
1. .357
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="taxon:112509"
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1. .357
/note="protein disulfide reductase; HvTrxh1"
/codon_start=1
/product="thiorodoxin h isoform 1"
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ORIGIN
Alignment Scores:
Pred. No.: 2.71e-31 Length: 357
Score: 338.00 Matches: 62
Percent Similarity: 71.19% Conservative: 22
Best Local Similarity: 52.54% Mismatches: 34
Query Match: 51.84% Indels: 0
DB: 8 Gaps: 0

US-10-005-429-14 (1-126) x AY245454 (1-357)
QY 1 MetAlaAGluGluGluValAlaValAlaCysHisThrLysAspGluPheAspAlaAarg 20
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QY 21 MetAlaLysAlaLysGluGluGluValValLysValValLysPheMetAlaProTyrCys 40
Db 61 ATGGCAATGTCGCAAGGACACCGGCAAGTGTGATGATGATTTCACTGCTTCCTGCTGC 120
QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db 121 GTCCATGTCGTGTCATGAGCCCGCTTCCTGATGACGACGCAAGAGTTCCTCGGCGCC 180
QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
Db 181 ATCTTCTGAAGTGTGATGATGAGCTGAAGGAGCTGCTGAAGCATCAATGTCGAG 240
QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db 241 GCAATGCGCGACCTTCCTTATTCATCAAGGACGCTGAGAGGAGGAGGACAGTGTGCGTGGC 300
QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaLysIleTyrThr 118
Db 301 AGGAGGATGATCATCCATCAAGATAGTGGCCCTCATGGGTTCTGCATCCACC 354

RESULT 8
AY072771
LOCUS Triticum aestivum cultivar Soissons thiorodoxin H mRNA, complete cds.
DEFINITION AY072771.1 GI:27461139
ACCESSION AY072771
VERSION AY072771.1
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
REFERENCE Cazalis,R.
AUTHORS Triticum aestivum thiorodoxin H
TITLE Unpublished
JOURNAL 2 (bases 1 to 598)
REFERENCE Cazalis,R.
AUTHORS Direct Submission
JOURNAL Submitted (10-JAN-2002) Plant Physiology, ESA Purpan, 75 voie du
TOEC, Toulouse 31076, France

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FEATURES

Location/Qualifiers
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CDS

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US-10-005-429-14 (1-126) x AY072771 (1-598)

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 QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProThrCys 40
 DB 61 ATGGCTAATGGCAAGGAGGAGCGGCAAGCTGGTATCAATGACTTCACTCTTCCTGGTGC 120
 QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
 DB 121 GGTCTTGTGCTATAGCCCGAGTCTTGTGATAGCCCAAGAGTTCCTGGCGC 180
 QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
 DB 181 ATTTCCTGAAGTGGACGTTGACGAGCTGAAGGACGCTGACATACACCAAGTTCGAG 240
 QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 DB 241 GCAATGCCGACCTTCTCTTTATCAAGGATGGTGGAGGTGGACACTTTGTCTGGTGGC 300
 QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla 120
 DB 301 AGAAGGATGATATCCATACCAAGATA-----GTGGCCCTCATGGTTCTGCATCTGCC 354

RESULT 9

AR414207
 LOCUS 466 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 1844 from patent US 6639063.
 ACCESSION AR414207
 VERSION AR414207.1 GI:40169317
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE

1 (bases 1 to 466)
 Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
 EST's and encoded human proteins
 JOURNAL Patent: US 6639063-A 1844 28-OCT-2003;

FEATURES

Location/Qualifiers
 1..466
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 2.08e-28 Length: 466
 Score: 315.00 Matches: 67
 Percent Similarity: 69.05% Conservative: 20
 Best Local Similarity: 53.17% Mismatches: 35
 Query Match: 48.31% Indels: 5
 DB: 6 Gaps: 1

US-10-005-429-14 (1-126) x AR414207 (1-466)

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 QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProThrCys 40
 DB 131 ATGACCAAGGCGGCAAGCTGGTGGTGCATCGACTTCACTGCCCGCTGGTGC 190
 QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
 DB 191 GT-CCATGCGCGCCCATCGCCCACTGTTCGACACGCGCCCAAGAGTTCCTAGGTGC 249
 QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
 DB 250 GTCTTCCTGAAGTGGACGTTGACGAGTGAAGGAGTCAACGCGCGCTTACGAGTCCGAG 309
 QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 DB 310 CGATGCGCGACCTTCCACTTCGTCAAGAACGCGCAAGCGGTGGCGACCATCGGTGGTGC 369
 QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla 120
 DB 370 AGAAGGAGGAGCTCTCTGCCCGAGTCCGAGGACATCGCGG-----CCTGGC 417
 QY 121 ProAlaSerAlaSerAla 126
 DB 418 CTTGCTCTGCGTCTGCC 435

RESULT 10

BD109760 466 bp DNA linear PAT 18-SEP-2002
 LOCUS
 DEFINITION EST and encoded human protein.
 ACCESSION BD109760
 VERSION BD109760.1 GI:23204578
 KEYWORDS JP 2002010789-A/1837.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 466)
 Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
 EST and encoded human protein
 Patent: JP 2002010789-A 1837 15-JAN-2002;
 GENSET CORP

COMMENT

OS Homo sapiens (human)
 PN JP 2002010789-A/1837
 PD 15-JAN-2002
 PF 07-AUG-2000 JP 2000280989
 PR 05-AUG-1999 US 60/147499
 PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
 GIORDANO
 PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
 C12N1/21,
 PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
 C12N15/00
 CC Von Heijne matrix
 CC score 4.30000019073486
 CC seq VVIDFTAAWCVHA/AP
 CC seq VVIDFTAAWCVHA/AP
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 FT CDS Location/Qualifiers
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 FT sig Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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ORIGIN
Alignment Scores:
Pred. No.: 2,08e-28 Length: 466
Score: 315.00 Matches: 67
Percent Similarity: 69.05% Conservativity: 20
Best Local Similarity: 53.17% Mismatches: 35
Query Match: 48.31% Indels: 5
DB: 6 Gaps: 1

US-10-005-429-14 (1-126) x BD109760 (1-466)
Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
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Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 131 ATGACCAAGGCCAGAGCGGCGAGCTGTGCTGCAACACGCGCAAGAGTTCACCTCAGGTC 190
Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db 191 GT-CCATCGCGCCGATCGCCCACTGTTCGTCGAACACGCGCAAGAGTTCACCTCAGGTC 249
Qy 61 ValPheLeuGluValAspValAspGluLeuValAlaLysIleTyrGlyValHis 80
Db 250 GTCTTCTCAGGTGAGCTGCGAGCTGCAAGTCAAGAGTCAACCGCGGCTCAGAGGTGCG 309
Qy 81 ValMetProThrPheCysPheIleArgAsnGlyLysLeuThrLeuGluSerPheAlaThrVal 100
Db 310 GCGATGCGGACCTTCCACTTCGTCAAGAACGCGCAAGCGTCCGCGCCATCGTGGTGCC 369
Qy 101 AspGluAspGluLeuArgAspAlaValAlaGlyLysTyrAlaAlaGlyThrThrAla 120
Db 370 AGAAGGACGAGCTCTCGCCAGATGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 417
Qy 121 ProAlaSerAlaSerAla 126
Db 418 CCTGCTGCTGCTGCTGCC 435

RESULT 11
AY088698 590 bp mRNA linear PLN 14-APR-2003
LOCUS Arabidopsis thaliana clone 9219 mRNA, complete sequence.
DEFINITION Arabidopsis thaliana clone 9219 mRNA, complete sequence.
ACCESSION AY088698
VERSION AY088698.1 GI:21407472
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 590)
Haas,B.J., Volforsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)
JOURNAL
MEDLINE 22088475
PUBMED 12093376
REFERENCE 2 (bases 1 to 590)
Brower,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
REFERENCE 3 (bases 1 to 590)
Brower,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
MALIBU, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
C-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the Ws or Laer ecotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
Genet carried out the library production and sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.
FEATURES
Location/Qualifiers
source 1..590
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/mol_type="mRNA"
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52..411
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CDS
2..83e-27 Length: 590
Score: 306.50 Matches: 60
Percent Similarity: 68.60% Conservativity: 23
Best Local Similarity: 49.59% Mismatches: 35
Query Match: 47.01% Indels: 3
DB: 8 Gaps: 2
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Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 52 ATGGCGCGCAGAGGCTCAAGTGTATGTTGTCACAGCAAGCATGTATGACGTGCA 111
Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 112 CTTGATAAAGCCAAAGAAATCCAAAGCTGATTGTGATTGATTCTACTGCTTCA 171
Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyr--ProSer 59
Db 172 CCACATGCGCGATGATGTTCCATTTTCAAGATTGCGCAAGAGTTCATGTCAGT 231
Qy 60 AlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVal 79
Db 232 GCCATCTTCTCAAGGTGGATGTTGATGAATCTCAGAGTGTGTTGCTAAAGAGT 291
Qy 80 HisValMetProThrPheCysPheIleArgAsnGlyLysLeuGluSerPheAlaThr 99
Db 292 GAGGCAATGCCAACCTTTGTTTCATTAAGCCGCGGAGTGTGGGAATAGCTGTTGT 351
Qy 100 ValAspGluAspGluLeuArgAspAlaValAlaGlyTyrAlaAlaGlyThrThr 119
Db 352 GCGAATAAAGAGATCTTCAGGCGGAAATAGTAGGACAT-----ACTGGTGT 405
Qy 120 Ala 120
Db 406 GCG 408
RESULT 12
AX505469

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AX505469	360 bp	DNA	linear	PAT 27-SEP-2002
LOCUS				
DEFINITION	Sequence 164 from Patent WO0216655.			
ACCESSION	AX505469			
VERSION	AX505469.1	GI:23386706		
KEYWORDS	Arabidopsis thaliana (thale cress)			
SOURCE	Arabidopsis thaliana			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE	1 Harper J.F., Kreps, J., Wang, X. and Zhu T. Stress-regulated genes of plants, transgenic plants containing same, and methods of use Patent: WO 0216655-A 164 28-FEB-2002; The Scripps Research Institute (US) ; Syngenta Participations AG (CH)			
JOURNAL				
FEATURES	Location/Qualifiers			
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Pred. No.:	305.50	Matches:	60	
Score:	67.7%	Conservative:	22	
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Query Match:	46.86%	Indels:	3	
DB:	6	Gaps:	2	
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Qy	21	MetAlaLysAlaLysGluClnuGlyLysLeuValIleAspPheMetAlaProTyrCys	40	
Db	61	CTTGATTAAGCCAAAGATCCAAACAGCTGATGTTGATTTTCACTGCTTCATGGT	120	
Qy	41	SerGlyCysGlnMetMetAlaProValTyrAlaLysCysAlaSerLysTyr---	59	
Db	121	CCACCATGCCGATGATGCTCCATTTTCAACGCTTTGGCGCAAGATTCATGTCAGT	180	
Qy	60	AlaValPheLeuClnuValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyVal	79	
Db	181	GCCTCTTTCTCAGGTGAGATGTTGATGACTTTCAGAGTGTGTGTAAGATTTGGTGTG	240	
Qy	80	HisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThr	99	
Db	241	GAGGCAATGCCAACCTTTGTGTTTCATTAAGCGCGGAAGTTGTGGATAGCTGCTTGGT	300	
Qy	100	ValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrThr	119	
Db	301	GCGAATAAGAGATCTTCAGCGCAAAATAGTGAAGCAT-----ACTGGGTGTACAACT	354	
Qy	120	Ala 120		
Db	355	GCG 357		
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BT004710				
LOCUS	BT004710	360 bp	mRNA	linear
DEFINITION	Arabidopsis thaliana Atg19730 gene, complete cds.			
ACCESSION	BT004710			
VERSION	BT004710.1	GI:28416850		
KEYWORDS	FLI CDNA			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			

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ORIGIN
Alignment Scores: 3.48e-27 Length: 556
Pred. No.: 305.50 Matches: 60
Score: 67.77% Conservative: 22
Percent Similarity: 49.59% Mismatches: 36
Best Local Similarity: 46.86% Indels: 3
Query Match: 8 Gaps: 2
DB:

US-10-005-429-14 (1-126) x AK118542 (1-556)

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Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProThrCys 40
Db 83 CTGTGATAAGCCAAAGAAATCCAAAGCTGATGTGATTCATCTCACTGCTTCATGGTGT 142
Qy 41 SerGlyCysGlnMetMetAlaProValTyAlaAspCysAlaSerLysTyr---ProSer 59
Db 143 CCACCATGCGCATGATGCTCCATTTCAACGATTGGCCAAAGATTCAATGCAAGT 202
Qy 60 AlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVal 79
Db 203 GCCATCTCTTCAAGTGGATGTTGATGAATTCAGAGTGTCTCTAAAGAGTTTGGTGTG 262
Qy 80 HisValMetProThrPheCysPheIleArgAsnGlyLthrLeuGluSerPheAlaThr 99
Db 263 GAGGCAATGCCAACCTTTGTTTCATTAAAGCCGGGAGATTGGATAGCTCGTTGGT 322
Qy 100 ValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThr 119
Db 323 GCGAATAAAGAGATCTTCAGCGCAAAATAGTGAAGCAT-----ACTGGTGTACAACT 376
Qy 120 Ala 120
Db 377 GCG 379

RESULT 15
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LOCUS A.thaliana (GREN) mRNA for thioredoxin. linear PLN 19-SEP-1995
DEFINITION A.thaliana (GREN) mRNA for thioredoxin.
ACCESSION Z35473
VERSION Z35473.1 GI:992959
KEYWORDS thioredoxin.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Rivera-Madrid,R., Meares,D., Marinho,P., Jacquot,J.P.,
Decottignies,P., Miginiac-Maslow,M. and Meyer,Y.
TITLE Evidence for five divergent thioredoxin h sequences in Arabidopsis
thaliana
JOURNAL PROC. Natl. Acad. Sci. U.S.A. 92 (12), 5620-5624 (1995)
MEDLINE 95296363
PUBMED 7777559

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Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 1 ATGGCGGAGAGAGGGTCAAGTGTGTTGTACACGAAACGATGATGACTGTGCAA 60
Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProThrCys 40
Db 61 CTGTGATAAGCCAAAGAAATCCAAAGCTGATGTGATTCATCTCACTGCTTCATGGTGT 120
Qy 41 SerGlyCysGlnMetMetAlaProValTyAlaAspCysAlaSerLysTyr---ProSer 59
Db 121 CCACCATGCGCATGATGCTCCATTTCAACGATTGGCCAAAGATTCAATGCAAGT 180
Qy 60 AlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVal 79
Db 181 GCCATCTCTTCAAGTGGATGTTGATGAATTCAGAGTGTGCTAAAGATTGGTGTG 240
Qy 80 HisValMetProThrPheCysPheIleArgAsnGlyLthrLeuGluSerPheAlaThr 99
Db 241 GAGGCAATGCCAACCTTTGTTTCATTAAAGCCGGGAGATTGGATAGCTCGTTGGT 300
Qy 100 ValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThr 119
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Qy 120 Ala 120
Db 355 GCG 357

RESULT 14
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LOCUS Arabidopsis thaliana At1g19730 mRNA for putative thioredoxin,
DEFINITION complete cds, clone: RAFL19-77-A10.
ACCESSION AK118542.1 GI:26452110
VERSION FLI CDNA; CAP trapper.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Seki,M., Iida,K., Satou,M., Sakurai,T., Akiyama,K., Ishida,J.,
Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Carninci,P.,
Kawai,J., Hayashizaki,Y. and Shinozaki,K.
TITLE Arabidopsis thaliana full-length cDNA
JOURNAL Published Only in Database (2002)
AUTHORS 2 (bases 1 to 556)
Seki,M., Iida,K., Satou,M., Sakurai,T., Akiyama,K., Ishida,J.,
Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Carninci,P.,
Kawai,J., Hayashizaki,Y. and Shinozaki,K.
Direct Submission
Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences
Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
230-0045, Japan (E-mail:mseki@gscl.riken.go.jp,
URL:http://pfigweb.gsc.riken.go.jp, Tel:81-45-503-9625,
Fax:81-45-503-9586)
COMMENT An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al. (1998) Plant J. 15:707-720;
Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et
al. (2001) Genomics 77:79-90) digested with BamHI and SalI.
This clone is in a modified phagescript vector.
Please visit our web site (http://pfigweb.gsc.riken.go.jp/) for
further details.
FEATURES
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1. .556
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REFERENCE 2 (bases 1 to 642)
AUTHORS Meyer, Y.
TITLE Direct Submission
JOURNAL Submitted (22-JUL-1994) Yves Meyer, Labo de Physio et Biol Mol
Vegetales, CNRS, URA 565, Av. de Villeneuve, Perpignan, 66860,
FRANCE

FEATURES
source Location/Qualifiers
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ORIGIN

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Query Match: 46.24% Indels: 3
DB: 8 Gaps: 2

US-10-005-429-14 (1-126) x ATTHIREDI (1-642)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 41 ATGGCGCCAGAGAGGGTCAAGTGATGGTTGTTCACACGACGATGATGAGCTGTGCAA 100
QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTyrCys 40
Db 101 CITGATAAGCCCAAGAAATCCAAACAGCTGATGTGATTTCACTGCTTCATGGTGT 160
QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyr---ProSer 59
Db 161 CCACCATGGCGCATGATGCTCCAAATTTCAACGATTTGCCCAAGAGATTCATGCACT 220
QY 60 AlaValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyVal 79
Db 221 GCCATCTTCTCAAGGTGATGTGATGAACCTTCAGAGTGTGCTAAAGAGTTTGGTGTG 280
QY 80 HisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThr 99
Db 281 GAGGCAATGCCAACCTTTGTGTTTCATTAAGCGCGCAAGTTGTGGATAAGCTCGTGTG 340
QY 100 ValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrThr 119
Db 341 GCGATAAAGAGAGATCTTCAGGCGGAAATAGTAGAGCAT-----ACTGGTGTTCACACT 394

Search completed: May 5, 2004, 04:56:23
Job time : 1528.27 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 00:59:23 ; Search time 162.118 Seconds
(without alignments)

3301.746 Million cell updates/sec

Title: US-10-005-429-14

Perfect score: 652

Sequence: 1 MAEEGAVIACHYKDEFDAR.....DAVRKYAAGCTTAPASASA 126

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=N_Geneseq_29Jan04 -QFWI=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blast62 -TRANS=human40.cgi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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8: Geneseq2003bs:.*
9: Geneseq2003cs:.*
10: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	361	55.4	540	9 ADC06863	Adc06863 Plasmid p
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3	361	55.4	686	2 AAQ78205	Aag78205 Gene codi
4	361	55.4	687	3 AAC66375	Aac66375 Rice thlo
5	333	51.1	659	3 ADC06860	Adc06860 Plasmid p
6	306.5	47.0	590	3 AAC38792	Aac38792 Arabidops
7	305.5	46.9	360	6 ABZ12359	Abz12359 Arabidops
8	285	43.7	3888	6 ABN9581	Abn9581 Phaseolin

9	285	43.7	3888	6	ABS53097	AbS53097 DNA encod
10	282.5	43.3	601	3	AAZ51740	Aaz51740 Glycine m
11	282	43.3	345	6	ABZ12358	Abz12358 Arabidops
12	282	43.3	345	6	ABN9587	Abn9587 Arabidops
13	282	43.3	561	3	AAC51522	Aac51522 Arabidops
14	282	43.3	561	3	AAC34121	Aac34121 Arabidops
15	282	43.3	3129	6	ABN9579	Abn9579 Phaseolin
16	282	43.3	3129	6	ABS53095	AbS53095 DNA encod
17	282	43.3	3888	6	ABN9580	Abn9580 Phaseolin
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19	279	42.8	470	3	AAC37781	Aac37781 Arabidops
20	275	42.2	738	3	AZ51739	Az51739 Glycine m
21	275	42.2	4935	6	ABN9586	Abn9586 Promoter-
22	267	41.0	509	5	AAH87768	Aah87768 Peppermin
23	265	40.6	574	3	AAZ51738	Aaz51738 Catalpa s
24	261	40.0	653	2	AAQ99783	Aaq99783 Plant SAR
25	261	40.0	653	2	AAV62799	Aav62799 Tobacco S
26	261	40.0	653	2	AAV81683	Aav81683 Tobacco p
27	260	39.9	614	3	AZ51741	Az51741 Vernonia
28	260	39.9	870	3	AAZ51737	Aaz51737 Momordica
29	254	39.0	366	7	ADA70643	Ada70643 Rice gene
30	253	38.8	393	2	AAT10451	Aat10451 Hard whea
31	253	38.8	393	2	AAC62457	Aac62457 Wheat thi
32	253	38.8	560	3	AAC41961	Aac41961 Arabidops
33	252.5	38.7	524	3	AAC33829	Aac33829 Arabidops
34	252	38.7	320	3	AA331785	Aa331785 Plant mic
35	252	38.7	328	3	AA331097	Aa331097 Plant mic
36	252	38.7	357	6	ABZ13931	Abz13931 Arabidops
37	252	38.7	357	7	ADA67904	Ada67904 Arabidops
38	252	38.7	480	3	AAC36542	Aac36542 Arabidops
39	252	38.7	563	3	AAC34211	Aac34211 Arabidops
40	252	38.7	576	7	ABX56868	Abx56868 Arabidops
41	252	38.7	652	3	AAC48656	Aac48656 Arabidops
42	251	38.5	369	3	AAC61537	Aac61537 Nucleotid
43	251	38.5	369	9	AAU59629	Aau59629 Barley th
44	249	38.2	382	3	AAC62456	Aac62456 Wheat thi
45	249	38.2	384	2	AAT10450	Aat10450 Soft whea

ALIGNMENTS

RESULT 1

ADC06863

ID ADC06863 standard; DNA; 540 BP.

XX

XX ADC06863;

XX

DT 18-DEC-2003 (first entry)

XX

DE Plasmid pDONR201 containing the modified rice thioresoxin H DNA.

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XX

XX

XX

PT Producing a modified, chimeric, or reconstructed DNA molecule of two
PT parts comprising amplifying the two DNAs by PCR using primers
PT incorporating recombination sites, ligating the PCR products, and then
PT cloning the ligated products.
XX
XX
XX Disclosure; Fig 5; 15pp; English.
XX
XX The invention relates to a novel method for producing a modified,
CC chimeric, or reconstructed DNA molecule composed of 2 parts. The method
CC comprises PCR amplification of each part using two primer sets that build
CC in recombination sites at the outer ends of each PCR product, ligating
CC the two PCR products and cloning the ligated products into a
CC recombination vector. The method of the invention may be useful for the
CC easy cloning and selection of chimeric DNA molecules. Unlike classical
CC recombination methods the new method avoids the need for initial cloning
CC using restriction enzymes and allows the production of mutated and/or
CC chimeric DNA molecules. The current sequence is that of the plasmid
CC pDONR201 of the invention which contains the modified rice thioresoxin H
CC DNA.
XX
XX Sequence 540 BP; 144 A; 130 C; 135 G; 131 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 4.2e-40 Length: 540
Score: 361.00 Matches: 70
Percent Similarity: 71.77% Conservatative: 19
Best Local Similarity: 56.45% Mismatches: 33
Query Match: 55.37% Indels: 2
DB: 9 Gaps: 1

US-10-005-429-14 (1-126) x ADC06863 (1-540)

QY 1 MetAlaAGluGluGlyAlaValIleAlaCyeshisthrlyAspGluPheAspAlaAZG 20
DB 58 ATGGCGCGGAGGAGGAGTGTGTATTCCTTCACACACAGGACGAGTTGACGCCAG 117
QY 21 MetAlaLysAlaLysGluGlnGlyLysValValIleAspPheMetAlaProTrpCys 40
DB 118 ATGACCAAGGCCAGGAGCGCGCAAAAGTGTCTATTAATTCACATTCCTCTGTGTGC 177
QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTrpProserAla 60
DB 178 GGACGTCGCCCTTCATCGCCCGAGTGTTCGTATACCCCAAAAGTCTCTGTGTGT 237
QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
DB 238 GTCCTCTGAGGTGATGTTGATGAGCTGAGGAGAGTCTCTGAAAGTACAATGTCCAG 297
QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
DB 298 GCAATGCCGACCTTCCTATTTCATCAAGATGTGTCTGAGGCTGACCAAGTGTGTGCCGCC 357
QY 101 AspGluAspGluLeuArgAspAlaValArgLysTrpAlaAlaAlaGlyThrThrAla 120
DB 358 AGGAGGATGACCTTCAGAAACACCATCGTGAAGAC-----GTCGGTGCACATGTGTGCA 411
QY 121 ProAlaSerAla 124
DB 412 TCTGCTTCTGCC 423

RESULT 2
ADC06864
ID ADC06864 standard; DNA; 660 BP.
XX
XX ADC06864;
XX
XX 18-DEC-2003 (first entry)
XX
XX Plasmid pDONR201 containing the rice thioresoxin H DNA - alternative.
DE
XX
XX cloning; recombination method; ds; plasmid pDONR201; rice; thioresoxin H.
XX
XX Unidentified.
CS

QY 121 ProAlaSerAla 124
 Db 484 TCTGCTTCTGCC 495

RESULT 3

AAQ78205
 ID AAQ78205 standard; cDNA; 686 BP.

XX AC AAQ78205;

DT 16-OCT-2003 (revised)

DT 13-JUL-1995 (first entry)

XX Gene coding for protein found in phloem sieve tube of rice.

XX Phloem sieve tube element; plant vascular bundle; rice;

KW protein transport; migration; fusion protein; ds.

XX Oryza sativa; (var. aichiasahi).

XX Key Location/Qualifiers

FT 5'UTR 1..56

FT /*tag= b

FT CDS 57..425

FT /*tag= a

FT 3'UTR 426..686

FT /*tag= c

XX JP06269286-A.

XX 27-SEP-1994.

XX 19-MAR-1993; 93JP-00060763.

XX 19-MAR-1993; 93JP-00060763.

XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.

XX WPI; 1994-346185/43.

XX P-PSDB; AAR65908.

XX Plant sieve tube protein gene - useful for transfer of useful proteins to the sieve tube.

XX Claim 1; Page 6; 13pp; Japanese.

XX Proteins obtained from the proboscis of a rice leaf hopper (Nilaparvata lugens Stal) were analysed; AAR65909 is the partial sequence of a fragment of a protein that is transported to the sieve tube. Based on this partial amino acid sequence, a probe (AAQ78206) was designed to screen for a sequence coding for the protein. A gene was cloned from the "aichiasahi" variety of rice (AAQ78205). By fusing the gene to a sequence coding for a second useful protein, the second protein will be transported to the sieve tube. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 686 BP; 170 A; 150 C; 182 G; 184 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5.92e-40 Length: 686
 Score: 361.00 Matches: 70
 Percent Similarity: 71.77% Conservative: 19
 Best Local Similarity: 56.45% Mismatches: 33
 Query Match: 55.37% Indels: 2
 DB: 2 Gaps: 1

US-10-005-429-14 (1-126) x AAQ78205 (1-686)

QY 1 MetAlaLysAlaGluGlnGlyValValIleAspPheMetAlaProTIPcys 20

Db 57 ATGCCCGCCGAGGAGGAGTGTGCTGCCTGCACCAACGAGGACGAGTTCGACGCCAG 116

QY 21 MetAlaLysAlaGluGlnGlyValValIleAspPheMetAlaProTIPcys 40
 Db 117 ATGCCCGCCGAGGAGGAGTGTGCTGCCTGCACCAACGAGTTCGACCTTCCTGCTGT 176
 QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerIleTyrProSerAla 60
 Db 177 GGCCTTGGCGTTCATCGCCCGCCAGTGTTCGCTGAATACGCCCAAAAGTTCCTGCTGCT 236
 QY 61 ValPheLeuGluValAspValAspGluLeuValValAlaLysIleTyrGlyValHis 80
 Db 237 GTCTTCTCGAGGTGATGTTGATGAGCTGAAGGAGTTCGCTGAAGGACATGATGCGAG 296
 QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 Db 297 GCAATGCCGACCTTCTATTTCATCAAGGATGTGCTGAGCTGACCAAGTTCGCTGGGCC 356
 QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
 Db 357 AGGAAGGATGACCTCCAGAACACCATCGTGAAGCAC-----GTCCGTGCCACTGCTGCA 410
 QY 121 ProAlaSerAla 124
 Db 411 TCTGCTTCTGCC 422

RESULT 4

AAQ66375

ID AAC66375 standard; cDNA; 687 BP.

XX AAC66375;

XX 23-FEB-2001 (first entry)

XX Rice thioredoxin h cDNA sequence.

XX Transformed plant; transfer protein; intercellular transfer;

XX thioredoxin h; rice; ss.

XX Oryza sativa.

XX Key Location/Qualifiers

FT CDS 57..425

FT /*tag= a

FT /product= "Thioredoxin h"

XX JP2000262169-A.

XX 26-SEP-2000.

XX 19-MAR-1999; 99JP-00074914.

XX 19-MAR-1999; 99JP-00074914.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2000-682116/67.

XX P-PSDB; AAB35810.

XX Transformed plants which can control the intercellular transfer of molecules using protoplasmic connections.

XX Example; Page 6-7; 8pp; Japanese.

XX This invention relates to a method for the production of a transformed plant which contains DNA which hybridises with DNA encoding a transfer protein. The transformed plant can control the intercellular transfer of a substance through the protoplasmic connections in the plant. The cDNA present sequence represents cDNA encoding rice thioredoxin h. The cDNA sequence is used in an example illustrating the method of the invention

XX SQ Sequence 687 BP; 171 A; 150 C; 182 G; 184 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5.93e-40 Length: 687

Score: 361.00 Matches: 70
Percent Similarity: 71.77% Conservative: 19
Best Local Similarity: 56.45% Mismatches: 33
Query Match: 55.37% Indels: 2
DB: 3 Gaps: 1

US-10-005-429-14 (1-126) x AAC66375 (1-687)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 57 ATGGCGCGGAGGAGGAGTCTGATCGCTCCCAACAAAGGAGGAGTTCGACCCGAG 116
QY 21 MetAlaLysAlaLysGluGluGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 117 ATGACCAAGCCAGGAGGCGGCAAGGGTCATATTGACTTCAGTCTCTCTGGTGT 176

QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerIleTyrProSerAla 60
Db 177 GGCCTTCGCGTTCATCGCCCGCAGTGTTCGCTGAATACGCCCAAAAGTTCCTGCTGT 236

QY 61 ValPheLeuGluValAspValAspGluLeuValAlaLysIleTyrGlyValHis 80
Db 237 GCTCTCTGAGGTTGATGTTGATGAGCTGAAGGAGTTGCTGAAAAGTACAAATGTCGAG 296

QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db 297 GCAATGCCGACCTTCCTATTTCATCAAGGATGCTGCTGAGGCTGACAAAGTCTGTCGCGCC 356

QY 101 AspGluAspGluLeuArgAspAlaValAlaGlyTyrAlaAlaGlyThrThrAla 120
Db 357 AGGAAGGATGAGCTCCAGAACACCATCTGTAAGGAC-----GTCGGTGCCACTGCTGCA 410

QY 121 ProAlaSerAla 124
Db 411 TCTGCTTCTGCC 422

RESULT 5
ADC06860
ID ADC06860 standard; DNA; 659 BP.
AC ADC06860;
DT 18-DEC-2003 (first entry)
DE Plasmid pDONR201 containing the rice thioedoxin H DNA.
XX clonig; recombination method; ds; plasmid pDONR201; rice; thioedoxin H.
XX Unidentified.
XX Oryza sativa.
XX US2003143618-A1.
XX 31-JUL-2003.
XX 23-JAN-2003; 2003US-00349782.
XX 23-JAN-2002; 2002EP-00075373.
XX (HATZ/) HATZFIELD Y.
XX (FRAN/) FRANKARD V M.
XX (DROU/) DROUAL A.
XX Hatzfield Y, Frankard VM, Droual A;
XX WPI; 2003-671205/63.
XX Producing a modified, chimeric, or reconstructed DNA molecule of two
XX parts comprises amplifying the two DNAs by PCR using primers
XX incorporating recombination sites, ligating the PCR products, and then
XX cloning the ligated products.
XX Disclosure; Page 7; 15pp; English.

XX The invention relates to a novel method for producing a modified,
CC chimeric, or reconstructed DNA molecule composed of 2 parts. The method
CC comprises PCR amplification of each part using two primer sets that build
CC in recombination sites at the outer ends of each PCR product, ligating
CC the two PCR products and cloning the ligated products into a
CC recombination vector. The method of the invention may be useful for the
CC easy cloning and selection of chimeric DNA molecules. Unlike classical
CC recombination methods the new method avoids the need for initial cloning
CC using restriction enzymes and allows the production of mutated and/or
CC chimeric DNA molecules. The current sequence is that of the plasmid
CC pDONR201 of the invention which contains the rice thioedoxin H DNA.
XX SQ Sequence 659 BP; 172 A; 159 C; 159 G; 169 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.16e-36 Length: 659
Score: 333.00 Matches: 69
Percent Similarity: 70.97% Conservative: 19
Best Local Similarity: 55.65% Mismatches: 34
Query Match: 51.07% Indels: 3
DB: 9 Gaps: 1

US-10-005-429-14 (1-126) x ADC06860 (1-659)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 130 ATGGCGCGGAGGAGGAGTCTGATCGCTCCCAACAAAGGAGGAGTTCGACCCGAG 189

QY 21 MetAlaLysAlaLysGluGluGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 190 ATGACCAAGCCAGGAGGCGGCAAGGGTCATATTGACTTCAGTCTCTCTGGTGT 249

QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerIleTyrProSerAla 60
Db 250 GGCCTTCGCGTTCATCGCCCGCAGTGTTCGCTGAATACGCCCAAAAGTTCCTGCTGT 309

QY 61 ValPheLeuGluValAspValAspGluLeuValAlaLysIleTyrGlyValHis 80
Db 310 GCTCTCTGAGGTTGATGTTGATGAGCTGAAGGAGTTGCTGAAAAGTACAAATGTCGAG 369

QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db 370 GCAATGCCGACCTTCCT-ATTATCAAGGATGCTGCTGAGGCTGACAAAGTCTGTCGCGCC 428

QY 101 AspGluAspGluLeuArgAspAlaValAlaGlyTyrAlaAlaGlyThrThrAla 120
Db 429 AGGAAGGATGAGCTCCAGAACACCATCTGTAAGGAC-----GTCGGTGCCACTGCTGCA 482

QY 121 ProAlaSerAla 124
Db 483 TCTGCTTCTGCC 494

RESULT 6
AAC38792
ID AAC38792 standard; DNA; 590 BP.
XX AAC38792;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 22248.
XX Hybridisation assay; Genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; 5S.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX

PF	25-FEB-2000;	2000EP-00301439.	
XX	25-FEB-1999;	99US-0121825P.	
PR	05-MAR-1999;	99US-0123130P.	
PR	08-MAR-1999;	99US-0123548P.	
PR	23-MAR-1999;	99US-0125788P.	
PR	25-MAR-1999;	99US-0126264P.	
PR	28-MAR-1999;	99US-0126785P.	
PR	01-APR-1999;	99US-0127462P.	
PR	06-APR-1999;	99US-0128234P.	
PR	08-APR-1999;	99US-0128714P.	
PR	16-APR-1999;	99US-0129645P.	
PR	19-APR-1999;	99US-0130077P.	
PR	21-APR-1999;	99US-0130449P.	
PR	23-APR-1999;	99US-0130510P.	
PR	24-APR-1999;	99US-0130891P.	
PR	28-APR-1999;	99US-0131449P.	
PR	30-APR-1999;	99US-0132048P.	
PR	30-APR-1999;	99US-0132407P.	
PR	04-MAY-1999;	99US-0132484P.	
PR	05-MAY-1999;	99US-0132485P.	
PR	06-MAY-1999;	99US-0132486P.	
PR	07-MAY-1999;	99US-0132487P.	
PR	07-MAY-1999;	99US-0132863P.	
PR	11-MAY-1999;	99US-0134256P.	
PR	14-MAY-1999;	99US-0134218P.	
PR	14-MAY-1999;	99US-0134219P.	
PR	14-MAY-1999;	99US-0134221P.	
PR	14-MAY-1999;	99US-0134370P.	
PR	18-MAY-1999;	99US-0134768P.	
PR	19-MAY-1999;	99US-0134941P.	
PR	20-MAY-1999;	99US-0135124P.	
PR	21-MAY-1999;	99US-0135353P.	
PR	21-MAY-1999;	99US-0135629P.	
PR	25-MAY-1999;	99US-0136021P.	
PR	27-MAY-1999;	99US-0136392P.	
PR	28-MAY-1999;	99US-0136782P.	
PR	01-JUN-1999;	99US-0137222P.	
PR	03-JUN-1999;	99US-0137528P.	
PR	04-JUN-1999;	99US-0137502P.	
PR	07-JUN-1999;	99US-0137724P.	
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PR	10-JUN-1999;	99US-0138847P.	
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PR	29-JUN-1999;	99US-0140991P.	
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PR	01-JUL-1999;	99US-0141842P.	
PR	01-JUL-1999;	99US-0142154P.	
PR	02-JUL-1999;	99US-0142055P.	
PR	06-JUL-1999;	99US-0142390P.	
PR	08-JUL-1999;	99US-0142803P.	
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PR	23-JUL-1999;	99US-0145224P.	
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PR	27-JUL-1999;	99US-0145913P.	
PR	27-JUL-1999;	99US-0145918P.	
PR	27-JUL-1999;	99US-0145919P.	
PR	28-JUL-1999;	99US-0145951P.	
PR	02-AUG-1999;	99US-0146386P.	
PR	02-AUG-1999;	99US-0146388P.	
PR	02-AUG-1999;	99US-0146389P.	
PR	03-AUG-1999;	99US-0147038P.	
PR	04-AUG-1999;	99US-0147204P.	
PR	04-AUG-1999;	99US-0147302P.	
PR	05-AUG-1999;	99US-0147192P.	
PR	05-AUG-1999;	99US-0147260P.	
PR	06-AUG-1999;	99US-0147303P.	
PR	06-AUG-1999;	99US-0147416P.	
PR	08-AUG-1999;	99US-0147493P.	
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PR	26-AUG-1999;	99US-0150884P.	
PR	27-AUG-1999;	99US-0151065P.	
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PR	30-AUG-1999;	99US-0151080P.	
PR	30-AUG-1999;	99US-0151303P.	
PR	31-AUG-1999;	99US-0151438P.	
PR	01-SEP-1999;	99US-0151930P.	
PR	07-SEP-1999;	99US-0152363P.	
PR	10-SEP-1999;	99US-0153070P.	
PR	13-SEP-1999;	99US-0153758P.	
PR	15-SEP-1999;	99US-0154018P.	
PR	16-SEP-1999;	99US-0154039P.	
PR	20-SEP-1999;	99US-0154779P.	
PR	22-SEP-1999;	99US-0155139P.	
PR	23-SEP-1999;	99US-0155486P.	
PR	24-SEP-1999;	99US-0155659P.	

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PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
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PR 08-OCT-1999; 99US-0158233P.
PR 12-OCT-1999; 99US-0158369P.
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PR 13-OCT-1999; 99US-0159295P.
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PR 21-OCT-1999; 99US-0160770P.
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PR 22-OCT-1999; 99US-0160981P.
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PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.
PR 29-OCT-1999; 99US-0162143P.

Alignment Scores:
Pred. No.: 1,64e-32
Score: 306.50
Percent Similarity: 68.60%
Best Local Similarity: 49.59%
Query Match: 47.01%
Indels: 3
Gaps: 2
DB: 3

US-10-005-429-14 (1-126) x AAC38792 (1-590)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
DB 52 ATGGCGGAGAGAGGGTCAAGTGAATTAGTTGTTCACAGACGATGTATGAGTGTGCA 111
QY 21 MetAlaAlaLysGluGluGlyLysLeuValIleAspPheMetAlaProTrpCys 40
DB 112 CTGTGATAAGCCAAAGATCCCAAGCTGATTGTGATTGATTCTCTCTCATGGTGT 171
QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyr---ProSer 59
DB 172 CCACCATGCGCGATGATTGCTCAATTTCAACGATTTGCCAAGAGTTCATGTCAGT 231
QY 60 AlavalPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVal 79
DB 232 GCCATCTTCTCAAGTGGTGTGTGATGAACCTTCAGAGTGTGCTAAAGAGTTTGTGTG 291
QY 80 HisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThr 99
DB 292 GAGGCAATGCCACCTTTGTTTCNTTAAGCCGCGGAGTTCGATTAAGCTCGTGTGT 351
QY 100 ValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaValGlyThrThr 119
DB 352 GCGAATAAAGAGATCTTCAGGCGGAAAATAGTGAAGCAT-----ACTGGTGTACACT 405
QY 120 Ala 120

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Db 406 GCG 408
RESULT 7
ABZ12359
ID ABZ12359 standard; DNA; 360 BP.
XX AC ABZ12359;
XX DT 21-JAN-2003 (first entry)
XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 164.
XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX OS Arabidopsis thaliana.
XX PN WO200216655-A2.
XX PD 28-FEB-2002.
XX PF 24-AUG-2001; 2001WO-US026685.
XX PR 24-AUG-2001; 2000US-0227866P.
XX PR 26-JUN-2001; 2001US-0264647P.
XX PR 22-JUN-2001; 2001US-0300111P.
XX (SCRI ) SCRIPPS RES INST.
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX Harper JF, Krepes J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX Identifying a stress condition to which a plant cell has been exposed and
XX producing plants with increased tolerance to these abiotic stresses.
XX Claim 144; SEQ ID NO 164; 577pp + Sequence Listing; English.
XX The invention relates to identifying a stress condition to which a plant
XX cell has been exposed, comprising: (a) contacting nucleic acid
XX representative of expressed polynucleotides in the plant cell with an
XX array or probes representative of the plant cell genome; and (b)
XX detecting a profile of expressed polynucleotides in the plant cell
XX characteristic of a stress response. The method is useful in the
XX production of transgenic plants, cells and seeds and in producing plants
XX with increased tolerance to abiotic stress. The present sequence is that
XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
XX in methods of the invention. Note: The sequence data for this patent is
XX not represented in the printed specification but is based on sequence
XX information supplied to Derwent by the European Patent Office
XX SQ Sequence 360 BP; 101 A; 64 C; 95 G; 100 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.11e-32
Score: 305.50
Percent Similarity: 67.77%
Best Local Similarity: 49.59%
Query Match: 46.86%
Indels: 3
Gaps: 2
DB: 6

US-10-005-429-14 (1-126) x ABZ12359 (1-360)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
DB 1 ATGGCGGAGAGAGGGTCAAGTGAATTAGTTGTTCACAGACGATGTATGAGTGTGCA 60
QY 21 MetAlaAlaLysGluGluGlyLysLeuValIleAspPheMetAlaProTrpCys 40
DB 61 CTGTGATAAGCCAAAGATCCCAAGCTGATTGTGATTGATTGATTGATTGATTGATTG 120
QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyr---ProSer 59

```

Db 121 CCACCATGCGCGATGATGTCCTCAATTTTCACAGATTGGCCAGAAAGTTCATGTCAGT 180
Qy 60 AlaValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyVal 79
Db 181 GCCATCTTCTCAAGTGGATGTTGATGAACTTCAGAGTGTTGCTAAAGAGTTTGTTGTTG 240
Qy 80 HisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThr 99
Db 241 GAGCAATGCCAACCTTTGTTGTTCAATTAAGCCGCGAAGTTGTGGATAAGCTGTTGGT 300
Qy 100 ValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrThr 119
Db 301 GCGAATAAGAGATCTTCAGCGAAATAAGTGAAGCAT-----ACTGGTGTACACT 354
Qy 120 Ala 120
Db 355 GCG 357
RESULT 8
ABN89581
ID ABN89581 standard; DNA; 3888 BP.
XX AC ABN89581;
XX DT 06-SEP-2002 (first entry)
XX DE Phaseolin promoter-Trxh oleosin-phaseolin terminator DNA SEQ:19.
XX KW Multimeric protein; redox protein; thiorodoxin; thiorodoxin reductase;
XX KW oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
XX KW vasotropic; vulnerary; antibacterial; immunosuppressive; antiulcer;
XX KW food product; milk; wheat; oxidative stress; cataract; diabetes;
XX KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
XX KW bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
XX KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
XX KW gastro oesophageal reflux disease; gene; ds.
XX OS Arabidopsis sp.
XX OS Phaseolus vulgaris.
XX PN WO200250289-A1.
XX PD 27-JUN-2002.
XX PF 19-DEC-2001; 2001WO-US050240.
XX PR 19-DEC-2000; 2000US-00742900.
XX PR 05-JUL-2001; 2001US-0302885P.
XX PR 04-DEC-2001; 2001US-00006038.
XX PA (SEMB-) SEMBIOSYS GENETICS INC.
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
PI Del Val G, Zaplachinski S, Moloney M;
XX DR WPI; 2002-508806/54.
XX DR P-PSDB; ABP60683.
XX PT Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.
XX PS Example 2; Page 169-171; 362pp; English.
XX CC The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant

CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, envenomation, bronchiolopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89581 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention
XX SQ Sequence 3888 BP; 1254 A; 722 C; 613 G; 1299 T; 0 U; 0 Other;

Alignment Scores: 2.33e-28 Length: 3888
Pred. No.: 285.00 Matches: 52
Score: 63.56% Conservative: 23
Percent Similarity: 44.07% Mismatches: 43
Best Local Similarity: 43.71% Indels: 0
Query Match: 6 Gaps: 0
DB:

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Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 1555 ATGGCTCGGAGAGAGGACAAAGTATCGCTGCCACACCGTTGAGACATGGAACGAGCAG 1614
Qy 21 MetAlaLysAlaLysGluGlnGlyLeuValIleAlaLysPheMetAlaProTyrCys 40
Db 1615 CTTCAGAAAGCTAATGAATCAAAACCTCTTGGTGGTGTATTCACGGCTCTTGGTGT 1674
Qy 41 SerGlyCysGlnMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db 1675 GGACCATGCTTTCATCGCTCCATCTTCTGCTGATTGGCTAAGAACTTCCTAACGTG 1734
Qy 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
Db 1735 CTTTTCTCAAGTTCATCTACTGATGATTAAGTTCGGTGGCAAGTCTTGGCGATACAG 1794
Qy 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db 1795 GCGATGCCAACCTTCATGTTTGAAGGAGGAGGAGATTTGGACAAGTTGTGGAGCC 1854
Qy 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThr 118
Db 1855 AAGAAGATGAGCTTCAGTCTACCATTTGCCAACACTTGGCTATGGCGGATACA 1908

RESULT 9

ABSS3097
ID ABSS3097 standard; DNA; 3888 BP.
XX AC ABSS3097;
XX DT 29-NOV-2002 (first entry)

XX DE DNA encoding Thiorodoxin-oleosin fusion protein.

XX KW Thiorodoxin; thiorodoxin reductase; gene expression; oleosin; oil body;
XX KW oleosin-thiorodoxin fusion protein; gene; ds.

XX OS Arabidopsis thaliana.

XX OS Brassica napus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT CDS 1555..2658

FT FT /*tag= a

FT FT /product= "Thiorodoxin-oleosin fusion protein"

FT FT 1555..2250

FT FT /*tag= b

FT FT /number= 1

FT FT 2251..2489

FT intron

Db 49 GAAGAGGAGCAGGTCAATCGCGCTCCACACCGTTGATGAGTGAAGTGCACAACTCCAGAAAT 108
 QY 24 AAlaYsGluGlnGlyLysLeuValValIleAAspPheMetAlaProThrPheCysSerGlyCys 43
 Db 109 GCAAAAGACTCCAAAAAGCTGATTTGGTGGATTTTACTCTTCTCTGGTGGTGGTCCATGC 168
 QY 44 GlnMetMetAlaProValThrAlaAAspCysAlaSerLysTyrProSerAlaValPheLeu 63
 Db 169 CGTTTATGCCCCAGTCTTTCGAGAGATTGCAAGAAACTCCTGAATTGATCTTCTC 228
 QY 64 GluValAspValAspGluLeuLeuGluValValAlaLysIleTyrGlyValHisValMetPro 83
 Db 229 AAGTGGATGTGATGAGTGAAGTGAAGTGGCTTGTCTGAGGAATATTCATTGAGGCCATGCCA 288
 QY 84 ThrPheCysPheIleArgAAspGlyGluThrLeuGluSerPheAlaThrValAlaAspGluAsp 103
 Db 289 ACCTTCTCTCTTGAAGATGGCGAGATCGTGGACAAGGTGGTGGTGGTGGTGGTGGTGGTGGT 348
 QY 104 GluLeuArgAspAlaValAlaGlyThrAlaAlaGlyThrThrThrThrThrThrThrThrThr 123
 Db 349 GACCTTCACGCCACCATGAGCAGCATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 399
 QY 124 AlaSer 125
 Db 400 TCTTCT 405
 RESULT 11
 ABZ12358
 ID ABZ12358 standard; DNA; 345 BP.
 AC ABZ12358;
 XX
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 163.
 XX
 XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 XX Arabidopsis thaliana.
 OS
 PN W0200216555-A2.
 XX
 XX
 PD 28-FEB-2002.
 XX
 XX
 PF 24-AUG-2001; 2001WO-US026685.
 XX
 XX 24-AUG-2000; 2000US-0227866P.
 PR 26-JAN-2001; 2001US-0264647P.
 PR 22-JUN-2001; 2001US-0300111P.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 XX Harper JF, Kreps J, Wang X, Zhu T;
 SI
 XX WPI; 2002-304127/34.
 XX
 XX Identifying a stress condition to which a plant cell has been exposed and
 PF producing plants with increased tolerance to these abiotic stresses.
 XX
 XX Claim 144; SEQ ID NO 163; 577pp + Sequence Listing; English.
 ES
 XX
 XX The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 CC in methods of the invention. Note: The sequence data for this patent is

CC not represented in the printed specification but is based on sequence
 CC information supplied to derwent by the European Patent Office
 XX
 SQ Sequence 345 BP; 90 A; 68 C; 90 G; 97 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1-85e-29 Length: 345
 Score: 282.00 Matches: 51
 Percent Similarity: 64.91% Conservative: 23
 Best Local Similarity: 44.74% Mismatches: 40
 Query Match: 43.25% Indels: 0
 DB: Gaps: 0
 US-10-005-429-14 (1-126) x ABZ12358 (1-345)
 QY 1 MetAlaAlaGluGluGlyAlaValIleAAspCysHisThrLysAspGluPheAspAlaArg 20
 Db 1 ATGCGTTCGAGAAAGACGACAGTGCCTGCCACACCGTTGAGAGCATGGAAACGAGCAG 60
 QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAAspPheMetAlaProThrPheCys 40
 Db 61 CTTCAAGAGCTAATCAATCCAAACTCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120
 QY 41 SerGlyCysGlnMetMetAlaProValThrAlaAspCysAlaSerLysTyrProSerAla 60
 Db 121 GGACCATGTCGTTTCATCGCTCCATCTTGTGCTGATTGGCTAAGAAACTTCCTCAACGG 180
 QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValValAlaLysIleTyrGlyValHis 80
 Db 181 CTTTCTCTCAAGTGTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 81 ValMetProThrPheCysPheIleArgAAspGlyGluThrLeuGluSerPheAlaThrVal 100
 Db 241 GCGATGCCAACCTTCATGTTTTTGAAGGAAGGAGAGATTTGGACAAAGTTGTGGAGCC 300
 QY 101 AspGluAspGluLeuArgAspAlaValAlaGlyThrLysTyrAlaAla 114
 Db 301 AAGAAAGATGAGCTTCAGTCTACCATTTGCCAAACACTGGCT 342
 RESULT 12
 ABN89587
 ID ABN89587 standard; DNA; 345 BP.
 XX
 AC ABN89587;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 XX Arabidopsis thaliana thioredoxin h (Trx h 1) DNA SEQ ID NO:38.
 DE
 XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KW oil body; ophthalmological; antidiabetic; cytosolic; antipariatic;
 KW vasotropic; vulnerary; antibacterial; immunosuppressive; antitumor;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease; gene; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 XX W0200250289-A1.
 PN
 XX
 XX 27-JUN-2002.
 XX
 XX 19-DEC-2001; 2001WO-US050240.
 PF
 XX 19-DEC-2000; 2000US-00742900.
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00006038.
 XX
 XX (SEMB-) SEMBIOYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX

PI Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 DR WPI; 2002-508806/54.
 DR P-PSDB; AAP60696.
 XX
 XX Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 XX Claim 68; Page 197; 362pp; English.
 XX
 XX The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABR89569 to ABR89593 and ABR60677 to
 CC ABR60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 XX SQ Sequence 345 BP; 90 A; 68 C; 90 G; 97 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,85e-29 Length: 345
 Score: 282.00 Matches: 51
 Percent Similarity: 64.91% Conservative: 23
 Best Local Similarity: 44.74% Mismatches: 40
 Query Match: 43.25% Indels: 0
 DB: 6 Gaps: 0
 US-10-005-429-14 (1-126) x ABR89587 (1-345)
 QY 1 MetAlaLaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 Db 1 ATGCTTCGGAAGAGCAAGTGATCGCTGCCACCGTTGAGACATGGAGCAGCAG 60
 QY 21 MetAlaLysAlaGlyGluGlnGlyLysLeuValValIleAspPheMetAlaProTrpCys 40
 Db 61 CTTCAGAGGCTAATGAATCCAAACTCTTGTTGGTGTGTTTTCACGGCTCTTGGTGT 120
 QY 41 SerGlyCysGlnMetAlaProValTyrAlaAspCysAlaSerIlystyrProSerAla 60
 Db 121 GGACCAATGCTTTCATCGCTCATCTTTCGATTCGGCTAAGAACTTCCTAACGTG 180
 QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
 Db 181 CTTTCTCTCAAGTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 Db 241 GCATGCTCAACCTTCATGTTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAla 114
 Db 301 AAGAAGATGAGCTTCAGTCTACCATTCATTCGCAACACATTCGCT 342
 RESULT 13
 AAC51522
 ID AAC51522 standard; DNA; 561 BP.
 XX
 XX AAC51522;
 , AC

XX 18-OCT-2000 (first entry)
 XX Arabidopsis thaliana DNA fragment SEQ ID NO: 68832.
 XX Arabidopsis thaliana.
 XX Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic pathway;
 KW promoter; termination sequence; ss.
 XX Arabidopsis thaliana.
 XX Arabidopsis thaliana.
 XX EPI033405-A2.
 XX 06-SEP-2000.
 XX 25-FEB-2000; 2000EP-00301439.
 XX 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
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 PR 30-APR-1999; 99US-0132407P.
 PR 04-MAY-1999; 99US-0132484P.
 PR 05-MAY-1999; 99US-0132485P.
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PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 20-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0150565P.
PR 26-AUG-1999; 99US-0150884P.

PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 13-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
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PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 28-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
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PR 13-OCT-1999; 99US-0159294P.
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PR 18-OCT-1999; 99US-0159584P.
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PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
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PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 26-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 3,72e-29
Score: 282.00
Percent Similarity: 64.91%
Best Local Similarity: 44.74%
Query Match: 43.25%
DB: 3

US-10-005-429-14 (1-126) x AAC51522 (1-561)

Qy 1 MetAlaAaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 94 ATGGCTTCGGAAGAGGACGAGTATCGCTGCCACCGTTGAGACATGGAACGAGCAG 153
Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTyrCys 40
Db 154 CTTTCAGAAAGCTTAATGAATCCAAACTCTTTGTGGTGGTATTTCACGGCTTCTTGTGT 213
Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db 214 GGACCATGTGCTTTCATCGCTCCATCTTTGCTGATTGCTAAGAACTTCCTAAGCTG 273

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QY 61 ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis 80
DB 274 CTTTTCCTCAAGGTGTACTGATGATTAAGTCGGTGGCAAGTATGGCGGTACAG 333
QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
DB 334 GCGATGCCAACCTTCATGTTTGAAGGAAGGAAGATTGGACAAAGTTGTTGGAGCC 393
QY 101 AspGluAspGluLeuArgAspAlaValAlaGlyTyrAlaAla 114
DB 394 AAGAAGATGACCTTCAGTCTACCATTCACCAACACTGGCT 435

RESULT 14
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ID AAC34121 standard; DNA; 563 BP.
XX
AC AAC34121;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 5524.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
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PR 05-MAR-1999; 99US-0123180P.
PR 03-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
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DB	156	CTTCGAGCGCTAATGATCCAAACTCTTGTGGGTGATTTACGGCTTCTTGGTGT 215		
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DB	276	CTTTTCCTCAAGGTGATCTGATGATTAAGTCGGTGGCAAGTATTGGGGGATACAG 335		
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DB	336	CGCATGCCAACCTTCATGTTTGAAGGAGGGAAGATTTCGACAAACTTCTGGAGCC 395		
QY	101	AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAla 114		
DB	396	AAGAAAGATGAGCTTCAGTCTACCATTCGCAAAACACTTGGCT 437		
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KW	Multimeric protein; redox protein; thioredoxin; thioredoxin reductase; oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic; KW vasotropic; vulnery; antibacterial; immunosuppressive; antitumor; KW food product; milk; wheat; oxidative stress; cataract; diabetes; KW chronic obstructive pulmonary disease; envenomation; sepsis; KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing; KW gastro intestinal bleeding; intestinal bowel disease; ulcer; KW gastro oesophageal reflux disease; Gene; ds.			
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OS	Arabidopsis sp.			
XX	Phaseolus vulgaris.			
PN	WO200250289-A1.			
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PD	27-JUN-2002.			
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PR	19-DEC-2000; 2000US-00742900.			
PR	05-JUL-2001; 2001US-0302885P.			
PR	04-DEC-2001; 2001US-00006038.			
XX	(SEMB-) SEMBIOSYS GENETICS INC.			
PA	(SYGN) SYNGENTA PARTICIPATIONS AG.			
XX				
PI	Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;			
PI	Del Val G, Zaplachinski S, Moloney M;			
XX				
DR	WPI; 2002-508806/54.			
DR	P-PSDB; ABF60680.			
XX	Producing oil body associated with recombinant multimeric protein complex			
PT				

PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
XX bodies.
XX
PS Example 2; Page 165-166; 362pp; English.
XX
CC The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention
XX
SQ Sequence 3129 BP; 1051 A; 549 C; 439 G; 1090 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,42e-28	Length:	3129
Score:	282.00	Matches:	51
Percent Similarity:	64.91%	Conservative:	23
Best Local Similarity:	44.74%	Mismatches:	40
Query Match:	43.25%	Indels:	0
DB:	6	Gaps:	0

US-10-005-429-14 (1-126) x ABN89579 (1-3129)

QY	1	MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg	20
DB	1555	ATGGCTTCGGAGAGGACAGATGTCGCTGCCACCGTTGAGACATGGAACGAGCAG	1614
QY	21	MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTrpCys	40
DB	1615	CTTCAGAGGCTAATGAATCCAAACTCTTGTGGTGTGATTTCACGGCTTCTTGGTGT	1674
QY	41	SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla	60
DB	1675	GGACCATGCGTTTCATCGCTTCATCTTGTGTTGCTAAGAACTCTTAACGTG	1734
QY	61	ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis	80
DB	1735	CTTTCTCCTCAAGGTTGATCTGATGAATCAAGTCGGTGGCAAGTGATTGGGGGATACAG	1794
QY	81	ValMetProThrPheCysPheIleArgAspGlyGluThrLeuGluSerPheAlaThrVal	100
DB	1795	GGCATGCCAACCTTCATGTTTGAAGGAGGAGATTTTGGACAAAGTTTGTGGAGCC	1854
QY	101	AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAla	114
DB	1855	AAGAAAGATGAGCTTCAGTCTACCATTCACCAACACTTCGCT	1896

Search completed: May 5, 2004, 03:24:14
Job time : 170.118 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 03:03:23 ; Search time 1168.74 Seconds
(without alignments)
3219.395 Million cell updates/sec

Title: US-10-005-429-14
Perfect score: 652
Sequence: 1 MAABEGAVIACHTKDEFDAR.....DAVRKYAAGTTTAPASASA 126

Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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16: em_estom.*
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27: em_gss_vrl.*
28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	621	95.2	427	14	CF647253 3530_1_41
5	618.5	94.9	568	14	CF020146 QB2B06.x
6	615.5	94.4	503	14	CF019553 QB1h06.x
7	615.5	94.4	504	14	CF019475 QB1h06.x
8	610	93.6	388	12	EG837010 Zm08_10f0
9	605.5	92.9	442	14	CD974597 QAB48B02.
10	600.5	92.1	411	14	CD976888 QAF23B09.
11	600.5	92.1	430	14	CD972346 QAE20B03.
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16	561.5	86.1	400	14	CD974844 QAB50C02.
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21	465.5	71.4	873	29	CG323435 OGWP320TV
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37	361	55.4	553	14	CF315555 HD--04-I0
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39	361	55.4	611	14	CF307434 HDA1--06-
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION QB16a01.xg QBI Zea mays cDNA clone QB16a01, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 496)

AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
 and <http://genoplante-info.infobiogen.fr>.

FEATURES

Location/Qualifiers
 1..496
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="P2"
 /db_xref="taxon:4577"
 /clone="QB16a01"
 /tissue_type="pedicel"
 /clone_lib="QB1"

ORIGIN

Alignment Scores:
 Pred. No.: 175e-69 Length: 496
 Score: 623.50 Matches: 126
 Percent Similarity: 98.44% Conservative: 0
 Best Local Similarity: 98.44% Mismatches: 0
 Query Match: 95.63% Indels: 2
 DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CF007324 (1-496)

QY 1 MetAlaAGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 DB 65 ATGGCGCGGAGGAGGTCGCGTATCGCGTGCACACCAAGAGCAGTTCGACGCCGC 124
 QY 21 MetAlaValAlaLysGluGlnGlyLysLeuValValIleAsp----PheMetAlaProTr 39
 DB 125 ATGGCAAGCCCAAGGAGGAGGTCGCGTATCGCGTGCACACCAAGAGCAGTTCGACGCCGC 184
 QY 39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
 DB 185 GTGCAGTGGTGCACAGATGATGCCCCCGGTGTACGGGAGCTGGCCAGCAAGTACCCCTTC 244
 QY 59 rAlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVa 79
 DB 245 CGCGGTCTCTCTCGAGTGCAGTGCAGCAACTGCTGGAAGTCGCGAAGATCTACGGCGT 304
 QY 79 lHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaTh 99
 DB 305 CCATGTGATGCCGACCTTCCTTCATCAGGAACGGGAGAGCTCGAGAGCTTTGCTTAC 364
 QY 99 rValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrTh 119
 DB 365 CGTCGACGAGGAGAGTCCGGGAGCGCGTCAGGAAGTACGCCGCCCTGGCACTACGAC 424
 QY 119 rAlaProAlaSerAlaSerAla 126
 DB 425 GGCTCTCTGCTCGCGGTCGCC 446

RESULT 2

CF019426
 LOCUS CF019426 503 bp mRNA linear EST 17-JUL-2003
 DEFINITION QB113c09.xg QB1 Zea mays cDNA clone QB19c09, mRNA sequence.
 ACCESSION CF019426
 VERSION CF019426.1 GI:32914614

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 503)

AUTHORS Genoplante.
 TITLE Genoplante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
 and <http://genoplante-info.infobiogen.fr>.

FEATURES

Location/Qualifiers
 1..503
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="P2"
 /db_xref="taxon:4577"
 /clone="QB19c09"
 /tissue_type="pedicel, whole kernel"
 /clone_lib="QB1"

ORIGIN

Alignment Scores:
 Pred. No.: 1.79e-69 Length: 503
 Score: 623.50 Matches: 126
 Percent Similarity: 98.44% Conservative: 0
 Best Local Similarity: 98.44% Mismatches: 0
 Query Match: 95.63% Indels: 2
 DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CF019426 (1-503)

QY 1 MetAlaAGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 DB 65 ATGGCGCGGAGGAGGTCGCGTATCGCGTGCACACCAAGAGCAGTTCGACGCCGC 124
 QY 21 MetAlaValAlaLysGluGlnGlyLysLeuValValIleAsp----PheMetAlaProTr 39
 DB 125 ATGGCAAGCCCAAGGAGGAGGTCGCGTATCGCGTGCACACCAAGAGCAGTTCGACGCCGC 184
 QY 39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
 DB 185 GTGCAGTGGTGCACAGATGATGCCCCCGGTGTACGGGAGCTGGCCAGCAAGTACCCCTTC 244
 QY 59 rAlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVa 79
 DB 245 CGCGGTCTCTCTCGAGTGCAGTGCAGCAACTGCTGGAAGTCGCGAAGATCTACGGCGT 304
 QY 79 lHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaTh 99
 DB 305 CCATGTGATGCCGACCTTCCTTCATCAGGAACGGGAGAGCTCGAGAGCTTTGCTTAC 364
 QY 99 rValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrTh 119
 DB 365 CGTCGACGAGGAGAGTCCGGGAGCGCGTCAGGAAGTACGCCGCCCTGGCACTACGAC 424
 QY 119 rAlaProAlaSerAlaSerAla 126
 DB 425 GGCTCTCTGCTCGCGGTCGCC 446

RESULT 3

CF005608
 LOCUS CF005608 562 bp mRNA linear EST 16-JUL-2003
 DEFINITION QB113b03.xg QB1 Zea mays cDNA clone QB113b03, mRNA sequence.
 ACCESSION CF005608
 VERSION CF005608.1 GI:32865926

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 562)

AUTHORS
TITLE
JOURNAL
COMMENT

Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante', (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).

FEATURES source

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1. .562
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QB113b03"
/tissue_type="pedicel"
/clone_lib="QBI"

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ORIGIN

Alignment Scores:		
Pred. No.:	2, 118-69	Length:
Score:	623.50	Matches:
Percent Similarity:	58.44%	Conservative:
Best Local Similarity:	58.44%	Mismatches:
Query Match:	95.63%	Indels:
DB:	14	Gaps:
		1
		562
		126

US-10-005-429-14 (1-126) X CF005608 (1-562)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
db 65 ATGGCGGCGGAGAGGGTGCGGTGATCGGTGCCACACAGGACGAGTTCGACGCCCG 124

Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAsp----PheMetAlaProTr 39
 125 ATGGCCAAAGGCCAAGGAGCAGGGCAAGCTGCTGGTCATCGACTTCTATGGCCCCCTG 184

Qy 39 pCysSerGlyCysClnMetMetAlaProValTyrAlaAspCysAlaSerIysTyrProSe 59
db 185 GTCAGTGGGTGCAGATGATGGCCCGGTACCGGACTCGGCAGCAGATACCTTC 244

Qy 59 rAlaValPheLeuGluValAspGluLeuValAlaLysIleTyrGlyVa 79
Db 245 cSGCGCTTCCTCCACGGCGCACGGCAAGCAGATCATACGGCT 304

Oy

79 LHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGlusSerPheaLath 99
|||||
Df 205 GCGTCTATCCGCACGGTCGTCTTGTTCAAGCCGCCAACCAGCCGCGAGCATTTCTACT 364

Qy 99 rValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrTh 119

Qy 119 rAlaProAlaSerAlaSerAla 126

RESULT 4
CF647253

DEFINITION 3530_141_1 D03.x.1 3530 - Full length cDNA library created by
Invitrogen from multiple tissues Zea mays cdNA, mRNA sequence.

ACCESSION CF647253

KEYWORDS	EST.
SOURCE	Zea mays
ORGANISM	Zea mays

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
1	(bases 1 to 427) Walbot,V. Maize ESTs from var University Unpublished (1999) Contact: Walbot V

Contact: Maxine
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Please: 3530 1 41 1 row: D column: 03.

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, indicating its effectiveness in predicting the target variable.	Model Performance Metrics
2. Robustness: The model demonstrates robustness against various input variations and noise, ensuring reliable predictions.	Model Performance Metrics
3. Interpretability: The model's predictions are interpretable, allowing users to understand the underlying factors influencing the outcome.	Model Performance Metrics
4. Scalability: The model is scalable, capable of handling large volumes of data and complex tasks efficiently.	Model Performance Metrics
5. Real-time Processing: The model is designed for real-time processing, enabling immediate decision-making based on incoming data.	Model Performance Metrics
6. Integration with Existing Systems: The model seamlessly integrates with existing systems, facilitating a smooth transition and adoption.	Model Performance Metrics
7. Customization: The model is highly customizable, allowing users to tailor it to specific requirements and use cases.	Model Performance Metrics
8. Security: The model adheres to strict security protocols, ensuring that data is protected and handled responsibly.	Model Performance Metrics
9. Compliance: The model complies with relevant regulatory requirements, ensuring legal and ethical standards are met.	Model Performance Metrics
10. Support and Maintenance: The model is supported by a dedicated team, ensuring timely updates, bug fixes, and user assistance.	Model Performance Metrics

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1. 427
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="multiple"
/dev_stage="varies by tissue"
/lab_host="DH108"
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/clone_lib=3530 - Full length cDNA library created by
 Nitrogen from multiple tissues"
 /note="Organ: silks, husks, ears, pollen, shoot tips,
 leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
 6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
 Project contracted with Invitrogen to produce a
 normalized, full length library in a p8top vector. This
 is a Gateway compatible vector, permitting clone movement
 to new vector backbones for expression in diverse host
 cells using recombination rather than restriction enzymes.
 Details of the vector and sequencing primers are available
 at ZmDB in the EST library description tables. poly(A)+
 mRNA was prepared by Invitrogen, and equimolar amounts of
 RNA from each of the 12 tissue samples were mixed together
 for selection of mRNA with a 5' cap. After synthesis of
 cDNA, a normalization step was conducted against the
 mixture of RNA sources. This step effected a 20X to 80X
 reduction in common transcript types. Tissues prepared: 1.
 just emerging silks; 2. inner husks from ears of sample
 #1; 3. 20 day aleurone; 4. immature tassels, stages from
 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
 vegetative shoot tips from 15 day old seedlings; all
 leaves with an expanded or partially expanded sheath
 were removed; 8. mature leaf tissue; 9. 0.5 cm long root
 tips from 15 day old seedlings; 10. 10 day whole seed; 11.
 12 day endosperm and embryo; 12. 17 day endosperm and
 embryo. All of the sequenced clones in project 3530 will
 be archived at the University of Arizona along with the
 unigene clones from the Maize Gene Discovery EST
 sequencing projects. Clones can be ordered through the
 ZmDB web site or directly from the University of Arizona
 (<http://www.genome.arizona.edu/orders/>). High density
 filters containing over 18,000 clones can also be ordered
 from the University of Arizona."

ORIGIN

Alignment Scores:		
Pred. No.:	2,938-69	Length:
Score:	621.00	Matches:
Percent Similarity:	98.35%	Conservative:
Best Local Similarity:	98.35%	Mismatches:
Query Match:	95.25%	Indels:
DB:	14	Gaps:
		0

US-10-005-429-14 (1-126) x CF647253 (1-427)

QY 1 MetAlaAaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 DB 64 ATGGCGCGAGGAGGAGTGGCGTATCGGTGGCCACCAAGGACGAGTTCGACGCCGC 123
 QY 21 MetAlaLysAlaLysGluGluGlyLysLeuValIleAspPheMetAlaProTrpCys 40


```

Db      124 ATGCCAAGCCAGGAGGAGGCGAAGCTGGTGTATCATGCTTCATGGCCCCCTGGTGC 183
Qy      41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db      184 AGTGGGTGCCAGATGATGGCCCCCGGTGTACGCGAGCTGCGCCAGCAAGTACCCCTTCGCGG 243
Qy      61 ValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHis 80
Db      244 GTCCTCTCTGAGGTGCGAGCTGGACCACTGCTGGAGTCCGAGATCTTACGGCGTCCAT 303
Qy      81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db      304 GTGATGCGGACCTTCTCTCTTCATCAGGAACGGGAGACGCTCGAGAGCTTTGCTACCGTC 363
Qy      101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
Db      364 GACGAGAGCAGCTCCGGGACGCGCTGAGGANTATCCCCCCCTGGCACTACGACGGCT 423
Qy      121 Pro 121
Db      424 CCT 426

RESULT 5
CF020146
LOCUS      568 bp mRNA linear EST 17-JUL-2003
DEFINITION QNZB06.XG QBN Zea mays cDNA clone QNZB06, mRNA sequence.
ACCESSION CF020146
VERSION    CF020146.1 GI:32915334
KEYWORDS  EST.
SOURCE    Zea mays
ORGANISM  Zea mays
REFERENCE  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE     clade; Panicoidae; Andropogoneae; Zea.
JOURNAL   1 (bases 1 to 568)
COMMENT   Genopiante.
          Genopiante, a major partnership french program in plant genomics
          Unpublished (2003)
          Contact: Genopiante
          Genopiante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genopiante' (http://www.genopiante.com
          and http://genopiante-info.infobiogen.fr).

FEATURES
         source
         1..568
            /organism="Zea mays"
            /mol_type="mRNA"
            /cultivar="F2"
            /db_xref="taxon:4577"
            /clone="QNZB06"
            /tissue_type="pedicel, whole kernel"
            /clone_lib="QBN"

ORIGIN
Alignment Scores:
Pred. No.:      9.37e-69      Length:      568
Score:          618.50      Matches:    125
Percent Similarity: 98.44%      Conservative: 1
Best Local Similarity: 97.66%      Mismatches: 0
Query Match:     94.86%      Indels:    2
DB:              14          Gaps:      1

US-10-005-429-14 (1-126) x CF020146 (1-568)
Qy      1 MetAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db      65 ATGGCGCCGAGGAGGCTGCGGTGATCGGTGTCACACCAAGGACGAGTTGACGCCCGC 124
Qy      21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAsp----PheMetAlaProTr 39

```

```

Db      125 ATGGCCAGGCGCAGGAGGAGGCGAAGCTGGTGTATCATGCTTCATGGCCCCCTG 184
Qy      39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
Db      185 GTCCAGTGGGTGCCAGATGATGGCCCCCGGTGTACGCGAGCTGCGCCAGCAAGTACCCCTTC 244
Qy      59 rAlaValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyVal 79
Db      245 CGCGGTCTTCTCGAGGTGCGAGCTGCGAGCACTGCTGGAAGTCCGGAAGATCTACGGCGCT 304
Qy      79 lHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaTh 99
Db      305 CCATGTGATGCGGACCTTCTCTTCATCAGGAACGGGAGACGCTCGAGAGCTTTGCTAC 364
Qy      99 rValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrTh 119
Db      365 CGTCAAGAGAGACGAGCTCCGGGACGCGCTGAGGAAGTACGCGCGCGCTGGCACTACGAC 424
Qy      119 rAlaProAlaSerAlaSerAla 126
Db      425 GGCTCTGCTGCTCGGCGTCCGCC 446

RESULT 6
CF019553
LOCUS      503 bp mRNA linear EST 17-JUL-2003
DEFINITION QBNih06.XG QBN Zea mays cDNA clone QBNih06, mRNA sequence.
ACCESSION CF019553
VERSION    CF019553.1 GI:32914741
KEYWORDS  EST.
SOURCE    Zea mays
ORGANISM  Zea mays
REFERENCE  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE     clade; Panicoidae; Andropogoneae; Zea.
JOURNAL   1 (bases 1 to 503)
COMMENT   Genopiante.
          Genopiante, a major partnership french program in plant genomics
          Unpublished (2003)
          Contact: Genopiante
          Genopiante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genopiante' (http://www.genopiante.com
          and http://genopiante-info.infobiogen.fr).

FEATURES
         source
         1..503
            /organism="Zea mays"
            /mol_type="mRNA"
            /cultivar="F2"
            /db_xref="taxon:4577"
            /clone="QBNih06"
            /tissue_type="pedicel, whole kernel"
            /clone_lib="QBN"

ORIGIN
Alignment Scores:
Pred. No.:      1.9e-68      Length:      503
Score:          615.50      Matches:    124
Percent Similarity: 97.66%      Conservative: 1
Best Local Similarity: 96.88%      Mismatches: 1
Query Match:     94.40%      Indels:    2
DB:              14          Gaps:      1

US-10-005-429-14 (1-126) x CF019553 (1-503)
Qy      1 MetAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db      65 ATGGCGCCGAGGAGGCTGCGGTGATCGGTGTCACACCAAGGACGAGTTGACGCCCGC 124
Qy      21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAsp----PheMetAlaProTr 39

```

```

Db      125 ATGCCAAGCCAGGAGGAGGCAAGCTGTGTTTCATCGACTTCGTTTCATGGCCCCCTG 184
Qy      39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
Db      185 GTGCAGTGGGTGGCCAGATGATGGCCCCGGGTGTACGGGAGCTGCGCCAGCAAGTACCCCTTC 244
Qy      59 rAlaValPheLeuGluValValAspValAspGluLeuGluValAlaLysIleTyrGlyVa 79
Db      245 CGCGGTCTTCTCGAGTTCGACGTCGACGAACCTCTCGAAGTCGCGAAGATCTACGGCGT 304
Qy      79 LHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaTh 99
Db      305 CCATGTGTATGCCGACCTTCTCTTCATCAGCAACGGGAGAGCTTCGAGAGCTTTGTCTAC 364
Qy      99 rValAspGluAspGluLeuArgAspAlaValAlaLysTyrAlaAlaGlyThrThrTh 119
Db      365 CGTCGACGAGGAGCTCCCGGACGCGTCAGGAGTACCGCCGCCCTGGCACTACGAC 424
Qy      119 rAlaProAlaSerAlaSerAla 126
Db      425 GGCTCTCTCGCTCGGCGTCCGCC 446

RESULT 7
CF019475      504 bp      mRNA      linear      EST 17-JUL-2003
LOCUS      QBN19405.xg QBN Zea mays cDNA clone QBN19405, mRNA sequence.
DEFINITION      CF019475
ACCESSION      CF019475
VERSION      CF019475.1 GI:32914663
KEYWORDS      EST.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 504)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.
Location/Qualifiers
FEATURES
source
1..504
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QBN19405"
/tissue_type="pedicel, whole kernel"
/clone_lib="QBN"

ORIGIN
Alignment Scores:
Pred. No.: 1.9e-68 Length: 504
Score: 615.50 Matches: 124
Percent Similarity: 97.66% Conservative: 1
Best Local Similarity: 96.88% Mismatches: 1
Query Match: 94.40% Indels: 2
DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CF019475 (1-504)

Qy      1 MetAlaAlaGluGluGluValAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db      64 ATGGCGGCGGAGGAGGTGGCGGTGATCGGTGCCACACCAAGGAGGAGTTCGACGCCGCG 123
Qy      21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAsp----PheMetAlaProThr 39

```

```

Db      124 ATGCCAAGCCAGGAGGAGGCAAGCTGTGTTTCATCGACTTCGTTTCATGGCCCCCTG 183
Qy      39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
Db      184 GTGCAGTGGGTGGCCAGATGATGGCCCCGGGTGTACGGGAGCTGCGCCAGCAAGTACCCCTTC 243
Qy      59 rAlaValPheLeuGluValValAspValAspGluLeuGluValAlaLysIleTyrGlyVa 79
Db      244 CGCGGTCTTCTCGAGTTCGACGTCGACGAACCTCTCGAAGTCGCGAAGATCTACGGCGT 303
Qy      79 LHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaTh 99
Db      304 CCATGTGTATGCCGACCTTCTCTTCATCAGCAACGGGAGAGCTTCGAGAGCTTTGTCTAC 363
Qy      99 rValAspGluAspGluLeuArgAspAlaValAlaLysTyrAlaAlaGlyThrThrTh 119
Db      364 CGTCGACGAGGAGCTCCCGGACGCGTCAGGAGTACCGCCGCCCTGGCACTACGAC 423
Qy      119 rAlaProAlaSerAlaSerAla 126
Db      424 GGCTCTCTCGCTCGGCGTCCGCC 445

RESULT 8
BG837010/c      388 bp      mRNA      linear      EST 25-MAY-2001
LOCUS      Zm08_10f04_A
DEFINITION      Zm08_AAF_C_ECORC_Fusarium graminearum inoculated_corn_ear Zea mays
cDNA clone Zm08_10f04, mRNA sequence.
ACCESSION      BG837010
VERSION      BG837010.1 GI:14203333
KEYWORDS      EST.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 388)
Harris,L.J. Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De
Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A.,
Spratt,D. and Tinker,N.A.
Expressed Sequence Tags from Developing Maize Kernels Six Days
after Silk Channel Inoculation with Fusarium graminearum
Unpublished (2001)
Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harris.lj@em.agr.ca.
Location/Qualifiers
FEATURES
source
1..388
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="CO430"
/db_xref="taxon:4577"
/clone="Zm08_10f04"
/tissue_type="Developing kernels (sibcrossed)"
/dev_stage="10-11 days post-silk emergence"
/clone_lib="Zm08_AAF_C_ECORC_Fusarium graminearum_inoculate
d_corn_ear"
/notes="vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;
Site_2: XhoI; Field-grown maize ears were silk
channel-inoculated in the morning (~10 am) with 1 ml of a
Fusarium graminearum macroconidial suspension (500,000
spores/ml) and whole ears were collected and immediately
frozen in liquid nitrogen 6 days later."

ORIGIN
Alignment Scores:
Pred. No.: 6.56e-68 Length: 388

```

Score:	610.00	Matches:	117
Percent Similarity:	59.16%	Conservative:	1
Best Local Similarity:	58.32%	Mismatches:	1
Query Match:	93.56%	Indels:	0
DB:	12	Gaps:	0
US-10-005-428-14 (1-126) x BG837010 (1-388)			
Qy	8	VallileAaCysHisThrLysAspGluPheAspAlaArgMetAlaLysAlaLysGluIn	27
Db	387	GTGATCGGTGCATACCAAGACGAGTTCAGACGCCCGCATGGCCAGGCCAAGAGGAG	328
Qy	28	GlyLysLeuValValIleAspPheMetAlaProThrCysSerGlyCysGlnMetMetAla	47
Db	327	GCACAGCTGGTGGTCATGCATTCATGCGCCCGCTGGTGGCTCCAGATCATGGCC	268
Qy	48	ProValTyrAlaAspCysAlaSerLysTyrProSerAlaValPheLeuGluValAspVal	67
Db	267	CCGGTGTACCGGACTGCGCCAGCAAGTACCTTTCGGCGGTCTTCTTCGAGGTTCGACGTC	208
Qy	68	AspGluLeuGluValAlaLysIleTyrGlyValHisValMetProThrPheCysPhe	87
Db	207	GACGAATCTCTGGAAGTCGCGAAGATCTACGGCGTCCATGTGATGCCAGCTTCTTCGCTTC	148
Qy	88	IleArgAsnGlyGluThrLeuGluSerPheAlaThrValAspGluAspGluLeuArgAsp	107
Db	147	ATCHGAAACGGGAGACGGCTCGAGAGCTTTGCTACCGTCCGACGAGGACGAGCTCCGGGAC	88
Qy	108	AlaValArgLysTyrAlaAlaAlaGlyThrThrThrAlaProAlaSerAlaSerAla	126
Db	87	GCCTGCAGAGGTACGCCGCCCTGGCACTACAGCGTCTCTGCGCTCGGGTCGCGC	31

RESULT 9	
CD974597/c	
LOCUS	442 bp mRNA linear EST 16-JUL-2003
DEFINITION	QAE48b02.yg QAE Zea mays cDNA clone QAE48b02, mRNA sequence.
ACCESSION	CD974597
VERSION	CD974597.1 GI:32834919
KEYWORDS	EST.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 442)
TITLE	Genopiante.
JOURNAL	Genopiante, a major partnership french program in plant genomics Unpublished (2003)
COMMENT	Contact: Genopiante Genopiante 93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10 This sequence has been generated in the framework of the french plant genomics programme 'Genopiante' (http://www.genopiante.com) and http://genopiante-info.infobiogen.fr .

```

FEATURES
source
1. .442
/organism="Zea mays"
/moi_type="mRNA"
/cultivar="R2"
/db_xref="taxon:4577"
/clone="QA348B02"
/tissue_type="pericarp"
/clone_lib="OAE"

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ORIGIN

Alignment Scores:		
Pred. No.:	3,016-67	Length: 442
Score:	605.50	Marches: 122
Percent Similarity:	97.66%	Conservative: 3
Best Local Similarity:	95.31%	Mismatches: 1
Query Match:	92.87%	Indels: 2

DB:	14	Gaps:	1
US-10-005-429-14	(1-126)	x	CD974597 (1-442)
Qy	1	MetAla	AlaGluGluGlyAlaValIleAlaC
Db	435	GTGCGGCCAAGGAGGGTCCGGTATCGCGTGCACCAAGGACGAGTTCAACGCCCGC	376
Qy	21	MetAla	AlaLysGluGlnGlyLeuValIleAsp----
Db	375	ATGCGCCAGGCCCAAGGAGCGAGGCAAGCTGGTGTCTATCGACTTCGTTCAITGGCCCCCTG	316
Qy	39	pCysSerGlyCysGlnMetMetalProValTyrAlaAspCysAlaSerLysTyrProSe	59
Db	315	GTCCAGTGGGTGCCAGATGATGGCCCGGTGTACGCGACTCGCCACCAAGTAGCCCTTC	256
Qy	59	rAlaVal	PhLeuGluValAspValAspGluLeuLeuValAlaLysIleTyrGlyVa
Db	255	CGCGGTCTTCTCTCGAGTTCGACGTCGACGAACTGCTGGAAGTCGCGAAGATCTACGGCGT	196
Qy	79	LHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaTh	99
Db	195	CCATGTGATGCCGACCTTTTGCTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTGCTTAC	136
Qy	99	rValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrTh	119
Db	135	CGTCGACGAGGACGAGCTCCGGGACGCCGTTCAGGAGGTACGCCCGCGCTGGCACTACGAC	76
Qy	119	rAlaProAlaSerAlaSerAla	126
Db	975	GGCTCTCTGGCTCGGCGTCCGCC	54

[illegible]

SOURCE

ORGANISM

800000

REFERENCES
AUTHORS

ETIT

JOURNAL

COMMENT

FEATURES

Source

SECRET

ORIGIN

Alignment

Pred. No.:

Score:

Percent Si

Best Local
Diner: Mot +

Y. Taniuchi

DB:	14	Gaps:	1
US-10-005-429-14	(1-126) x CD972346 (1-430)		
Qy	6	GlyAlaValIleAlaCySHisThrLysAspGluPheAspAlaArgMetAlaLysAlaLys	25
Db	3	GSGTCCGTGATCGGTGCCACACCAAGACGAGTTGACGCCCGCATCGCCCAAGCCCAAG	62
Qy	26	GlulGlnGlyLysLeuValValIleAsp----	44
Db	63	GAGCAGGGCAAGCTGGTGGTCATCGATTCTGATGGCCCTTGGTCCAGTGGGTGCCA	122
Qy	44	nMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaValPheLeuGl	64
Db	123	GATGATGGCCCGCGGTGTACGGGACTCGCCAGCAAGTACCTTCCGGGGCTTCTCTCGA	182
Qy	64	uValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHisValMetProTh	84
Db	183	GGTCGAGCTCGACGAAGCTGCTGGAAGTGGGAGATCTACGGCGTCCCATGTGATGCCGAC	242
Qy	84	rPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValAspGluAspGl	104
Db	243	CTTCTGTTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTGCTACCGTCCGAGGACGA	302
Qy	104	uLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrThrAlaProAlaSerAl	124
Db	303	GCTCCGGAGCGCGCTCAGGAAGTACGCCGCCGCTGGCACTACGACGGCTCTCTGCTCGCC	362
Qy	124	aSerAla	126
Db	363	GTCCGCC	369

RESULT 12	
CD978907	480 bp mRNA linear EST 16-JUL-2003
LOCUS	
DEFINITION	QAF6F04.YG QAF Zea mays cDNA clone QAF6F04, mRNA sequence.
ACCESSION	CD978907
VERSION	CD978907.1 GI:32839226
KEYWORDS	EST.
SOURCE	Zea mays
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 480)
AUTHORS	Genoplatte.
TITLE	Genoplatte, a major partnership french program in plant genomics
JOURNAL	Unpublished (2003)
COMMENT	Contact: Genoplatte Genoplatte 93, rue Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10 This sequence has been generated in the framework of the french plant genomics programme 'Genoplatte' (http://www.genoplatte.com and http://genoplatte-info.infobiogen.fr).

```

FEATURES
  source
    Location/Qualifiers
      1..480
        /organism="Zea mays"
        /mol_type="mRNA"
        /cultivar="F2"
        /db_xref="taxon:4577"
        /clone="QAF6f04"
        /tissue_type="pericarp"
        /clone_lib="QAF"

ORIGIN

Alignment Scores:
Pred. No.: 1.49e-66
Score: 600.50
Percent Similarity: 98.37%
Best Local Similarity: 98.37%
Query Match: 92.10%

Length: 480
Matches: 121
Conservative: 0
Mismatch: 0
Indels: 2

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DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CD978907 (1-480)

QY 6 GlyAlaValIleAlaCysHisThrIysAspGluPheAspAlaArgMetAlaIysAlaLys 25

DB 3 GGTGGCGTGCATCGCGTGCACACCAAGGACGAGTTCGACGCCCGCATGCCAAGCCCAAG 62

QY 26 GluGlnGlyLysLeuValIleAsp----PheValAlaProTyrCysSerGlyCysCl 44

DB 63 GAGCAGGGCAAGCTGTGTGTCTGTCATGCGCCCTGTGTGAGTGGTGGTGGCA 122

QY 44 nMetMetAlaProValTyrAlaAspCysAlaSerIysTyrProSerAlaValPheLeuGl 64

DB 123 GATGATGGCCCGGTGTACCGGACTGCGCCAGGATACCTTCGCGGTCTTCTCTGA 182

QY 64 uValAspValAspGluLeuGluValAlaLysIleTyrGlyValHisValMetProTh 84

DB 183 GGTGACGTCGACGAATCTGTGAGTCCGAGATCTACGGCGTCCATGTATGCCGAC 242

QY 84 rPheCysPheIleArgAsnGlyLysLeuGluSerPheAlaThrValAspGluAspGl 104

DB 243 CTCTCTCTTCATCAGGACGCGGAGAGCTCGAGCTTGTACCGTGCAGGAGCA 302

QY 104 uLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAlaProAlaSerAl 124

DB 303 GCTCCGGGACGGCTCAGCAAGTACGCCCGCGTGGCACTAGCAGCGCTCTGCTCGGC 362

QY 124 aSerAla 126

DB 363 GTCCGCGC 369

RESULT 13

BG837151/c

LOCUS

DEFINITION

Zm08_06b07 A 456 bp mRNA linear EST 25-MAY-2001

Zm08_AAFc_ECORC_Fusarium_graminearum_inoculated_corn_ear Zea mays

CDNA clone Zm08_06b07, mRNA sequence.

ACCESSION

BG837151

VERSION

BG837151.1 GI:14203474

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 456)

Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S., Singh,J.A., Spratt,D., and Tinker,N.A.

Expressed Sequence Tags from Developing Maize Kernels Six Days after Silk Channel Inoculation with Fusarium graminearum

Unpublished (2001)

Contact: Harris, Linda J.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada

Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA

Tel: (613) 759-1314

Fax: (613) 759-6566

Email: harrisl@em.agr.ca.

Location/Qualifiers

1..456

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="CO430"

/db_xref="taxon:4577"

/clone="Zm08_06b07"

/tissue_type="Developing kernels (sibcrossed)"

/dev_stage="10-11 days post-silk emergence"

/clone_1lib="Zm08_AAFc_ECORC_Fusarium_graminearum_inoculate d_corn_ear"

/note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;

FEATURES

source

1..456

Location/Qualifiers

1..456

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="F2"

/db_xref="taxon:4577"

/clone="QBI7d05"

/tissue_type="pedicel"

ORIGIN

Alignment Scores:

Pred. No.: 5,89e-64 Length: 456

Score: 580.00 Matches: 114

Percent Similarity: 95.83% Conservative: 1

Best Local Similarity: 95.00% Mismatches: 4

Query Match: 88.96% Indels: 1

DB: 12 Gaps: 0

US-10-005-429-14 (1-126) x BG837151 (1-456)

QY 1 MetAlaAlaGluGlyAlaValIleAlaCysHisThrIysAspGluPheAspAlaArg 20

DB 369 ATGGCGCGGAGGAGGGTGGCGGTGATCGCGTCCATACCAAGGACGAGTTCGACCCCGC 310

QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40

DB 309 ATGGCCAGGCCCAAGGAGGAGGCAAGCTGTGGTTCATCGACTTCATGGCCCTGTGTC 250

QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerIysTyrProSerAla 60

DB 249 AGTGGGTGCCAGATGATGCGCCCGTGTACCGGACTGCGCGAGTCCGCAAGTACCTTCCCGC 190

QY 61 ValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHis 80

DB 189 GTCTTCCTCGAGTTCGAGTTCGAGCACTGCTGGAGTTCGCGAGATCTACGGGTCCAT 130

QY 81 ValMetProThrPheCysPheIleArgAsnGlyLysLeuGluSerPheAlaThrVal 100

DB 129 GTGATGCCGAGCTTCTGCTTCATCAGGAACGCGGAGACGCTCGAGAGCTTTGCTACCGTC 70

QY 101 AspGluAspGluLeu-ArgAspAlaValArgLysTyrAlaAlaGlyThrThr 119

DB 69 GACGAGGACGAGCTHCCGCGACGCCGTGCGAGTACGACACGCGCTGGCAACTACA 12

RESULT 14

CF008093

LOCUS

DEFINITION

QBI7d05.xg QBI Zea mays cDNA clone QBI7d05, mRNA sequence.

ACCESSION

CF008093

VERSION

CF008093.1 GI:32868411

KEYWORDS

EST.

SOURCE

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 426)

Genoplante.

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.

Location/Qualifiers

1..426

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="F2"

/db_xref="taxon:4577"

/clone="QBI7d05"

/tissue_type="pedicel"

FEATURES

source

1..426

Location/Qualifiers

1..426

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="F2"

/db_xref="taxon:4577"

/clone="QBI7d05"

/tissue_type="pedicel"

Site 2: XhoI; Field-grown maize ears were silk channel-inoculated in the morning (~10 am) with 1 ml of a Fusarium graminearum macroconidial suspension (500,000 spores/ml) and whole ears were collected and immediately frozen in liquid nitrogen 6 days later."

/clone_lib="QBI"

ORIGIN

Alignment Scores:

Pred. No.: 2,7e-63 Length: 426
 Score: 574.50 Matches: 116
 Percent Similarity: 96.69% Conservatives: 1
 Best Local Similarity: 95.87% Mismatches: 2
 Query Match: 88.11% Indels: 2
 DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CF008093 (1-426)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 DB 66 ATGGCGCCGAGGAGGTCGGTGCATCGCTGCCACCAAGGAGGTCGAGTCGAGCGCGC 125
 QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPhe-----MetAlaProTr 39
 DB 126 ATGGCCCAAGCCCAAGGAGGCAAGCTGTCATCGACTTCGGTCTCATGCGCCCGCCCTG 185
 QY 39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
 DB 186 GTGCAGTGGGTGCCAGATGATGGCCCCGGTGTCAGCGGATGTGCCAGCAAGTACCCCTTC 245
 QY 59 rAlaValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyVa 79
 DB 246 CGCGGTCTTCTCGAGTCGAGTCGACGAACTGCTCGAAGTCGCGAAGATCTACGCGGT 305
 QY 79 lHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaTh 99
 DB 306 CCATGTGATGCCGACCTTCCTTCATCAGGAACGGGAGCGCTCGAGAGCTTTGCTAC 365
 QY 99 rValAspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrTh 119
 DB 366 CFTCGACGAGGACGAGCTCCGGACGCGCTCAGGAAGTCGCGCGCGCTGCGACTACGAC 425
 QY 119 r 119
 DB 426 G 426

RESULT 15

CF006552 573 bp mRNA linear EST 16-JUL-2003
 LOCUS QBI20e10.xg QBI Zea mays cDNA clone QBI20e10, mRNA sequence.

DEFINITION CF006552
 ACCESSION CF006552
 VERSION CF006552.1 GI:32866870
 KEYWORDS EST.

SOURCE

Zea mays
 ORGANISM Zea mays
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
 Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACAD
 clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 573)

REFERENCE

1 Genopiante.
 Genopiante, a major partnership french program in plant genomics
 Unpublished (2003)

AUTHORS

CONTACT: Genopiante
 Genopiante
 93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
 plant genomics programme 'Genopiante' (<http://www.genopiante.com>)
 and <http://genopiante-info.inbioogen.fr>.

FEATURES

1..573
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultiVar="F2"
 /db_xref="taxon:4577"
 /clone="QBI20e10"
 /tissue_type="pedicel"

ORIGIN

/clone_lib="QBI"

Alignment Scores:

Pred. No.: 2,46e-62 Length: 573
 Score: 568.50 Matches: 123
 Percent Similarity: 93.89% Conservatives: 0
 Best Local Similarity: 93.89% Mismatches: 3
 Query Match: 87.19% Indels: 5
 DB: 14 Gaps: 1

US-10-005-429-14 (1-126) x CF006552 (1-573)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 DB 65 ATGGCGCCGAGGAGGTCGGTGCATCGCTGCCACCAAGGAGGTCGAGTCGAGCGCGC 124
 QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAsp-----PheMetAlaProTr 39
 DB 125 ATGGCCCAAGCCCAAGGAGGCAAGCTGTCATCGACTTCGGTCTCATGCGCCCGCCCTG 184
 QY 39 pCysSerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSe 59
 DB 185 GTGCAGTGGGTGCCAGATGATGGCCCCGGTGTCAGCGGACTGCGCCAGCAAGTACCCCTTC 244
 QY 59 rAlaValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyVa 79
 DB 245 CGCGGTCTTCTCGAGTCGAGTCGACGAACTGCTCGAAGTCGCGAAGATCTACGCGGT 304
 QY 79 lHisValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPhe-AlaT 99
 DB 305 CCATGTGATGCCGACCTTCTGCTTCATCAGGAACGGGAGAGCGCTCGAGAGCTTTGCTTA 364
 QY 99 hrValAsp-GluAspGluLeuArg-AspAlaValArgLysTyrAlaAlaGlyThrTh 118
 DB 365 CCGGCGACGAGGACGAGCTCCGGGAGCGCGTCAGGAAGTACGCGCGCGCTGGCACTAC 424
 QY 118 rThrAlaProAlaSerAlaSerAla 126
 DB 425 GACGGCTCTCTGCTCGCGGTTCGCCC 449

Search completed: May 5, 2004, 06:07:22

Job time : 1182.74 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 03:14:43 ; Search time 36.3939 Seconds
(without alignments)
1921.307 Million cell updates/sec

Title: US-10-005-429-14

Perfect score: 652
Sequence: 1 MAEEGAVIACHIKDEPDAR.....DAVRKYAAGTTTAPASASA 126

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Rgapop 6.0, Rgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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4: /cgn2_6/ptodata/2/ina/6B COMB seq.*
5: /cgn2_6/ptodata/2/ina/pctus COMB seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315	48.3	466	4	US-09-621-976-1844
2	261	40.0	653	1	US-08-181-271A-103
3	261	40.0	653	1	US-08-449-315-103
4	261	40.0	653	1	US-08-444-803-103
5	261	40.0	653	1	US-08-449-043-103
6	261	40.0	653	1	US-08-456-265A-103
7	261	40.0	653	1	US-08-455-416-103
8	261	40.0	653	1	US-08-455-244-103
9	261	40.0	653	1	US-08-454-876-103
10	261	40.0	653	2	US-08-457-364-103
11	261	40.0	653	2	US-08-456-262-103
12	261	40.0	653	2	US-08-456-240-103

13	261	40.0	553	2	US-08-455-736-103	Sequence 103, App
14	261	40.0	553	2	US-08-971-217-103	Sequence 103, App
15	261	40.0	553	3	US-09-350-600-103	Sequence 103, App
16	261	40.0	553	4	US-09-906-234-103	Sequence 103, App
17	253	38.8	393	4	US-09-540-014-5	Sequence 5, Appli
18	251	38.5	369	4	US-09-540-014-1	Sequence 1, Appli
19	249	38.2	382	4	US-09-540-014-3	Sequence 3, Appli
20	232.5	35.7	318	4	US-09-313-294A-5868	Sequence 5868, Ap
21	208	31.9	278	4	US-09-313-294A-5840	Sequence 5840, Ap
22	178	27.3	557	4	US-09-404-879A-88	Sequence 88, Appl
23	178	27.3	557	4	US-09-338-933-88	Sequence 88, Appl
24	178	27.3	557	4	US-09-215-681-88	Sequence 88, Appl
25	178	27.3	557	4	US-09-216-003A-88	Sequence 88, Appl
26	178	27.3	581	4	US-09-601-144-67	Sequence 67, Appl
27	178	27.3	594	4	US-09-404-879A-87	Sequence 87, Appl
28	178	27.3	594	4	US-09-338-933-87	Sequence 87, Appl
29	178	27.3	594	4	US-09-215-681-87	Sequence 87, Appl
30	178	27.3	594	4	US-09-216-003A-87	Sequence 87, Appl
31	178	27.3	601	4	US-09-404-879A-133	Sequence 133, App
32	178	27.3	601	4	US-09-338-933-133	Sequence 133, App
33	178	27.3	601	4	US-09-215-681-133	Sequence 133, App
34	178	27.3	601	4	US-09-216-003A-133	Sequence 133, App
35	178	27.3	624	3	US-09-385-982-526	Sequence 526, App
36	178	27.3	630	3	US-08-180-371-5	Sequence 5, Appli
37	178	27.3	630	3	US-08-180-371-17	Sequence 17, Appl
38	178	27.3	630	5	PCT-US92-05707-5	Sequence 5, Appli
39	172	26.4	805	3	US-09-385-982-485	Sequence 485, App
40	161	24.7	2454	1	US-07-872-673B-1	Sequence 1, Appli
41	160.5	24.6	1545	1	US-07-872-673B-2	Sequence 2, Appli
42	160	24.5	631	3	US-09-385-982-174	Sequence 174, App
43	156.5	24.0	7096	4	US-09-221-017B-373	Sequence 373, App
44	154	23.6	1696	4	US-09-198-603C-3	Sequence 3, Appli
45	147.5	22.6	914	1	US-08-386-729A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-1844
; Sequence 1844, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1844
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 71..256
; NAME/KEY: sig peptide
; LOCATION: 71..199
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.30000019073486
; OTHER INFORMATION: seq VVIDFTAAACVHA/AP
US-09-621-976-1844

Alignment Scores:
Pred. No.: 1.58e-35
Score: 315.00
Percent Similarity: 69.05%
Best Local Similarity: 53.17%
Query Match: 48.31%
DB: 4
Length: 466
Matches: 67
Conservative: 20
Mismatches: 35
Indels: 5
Gaps: 1

Qy 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
Db 189 CCTTGGCGTTTATGCCCCCAATCTTCTGACATTCCTAAGAGATGCCCATGTATA 248
Qy 62 PheLeuGluValAspValAspGluLeuLeuGluValAla-LysIleTyrGlyValHisVa 81
Db 249 TTCCTCAAGCTTGATGTGTGATGAACCTGAGACTGTTTCAGCGGAATGGAGTGGAGGC 308
Qy 81 lMetProThrPheCysPheIleArgAenGlyGluThrLeuGluSerPheAlaThrValAs 101
Db 309 AATGCCAATTTTCTTCTTATTAAGATGAAGAGAGTGCAGAGATGTTGGTGCCTAA 368
Qy 101 pGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
Db 369 GAAAGAGAGTTCAGCAGACCATAGTGAAGCATGCTCTCTGCTACTGCTACTGCT 426

RESULT 3

US-08-449-315-103

Sequence 103, Application US/08449315

Patent No. 5650505

GENERAL INFORMATION:

APPLICANT: Ryals, John A.

APPLICANT: Alexander, Danny C.

APPLICANT: Beck, James J.

APPLICANT: Duesing, John H.

APPLICANT: Friedrich, Leslie B.

APPLICANT: Goodman, Robert M.

APPLICANT: Harms, Christian

APPLICANT: Meins, Jr. Frederick

APPLICANT: Montoya, Alice

APPLICANT: Moyer, Mary B.

APPLICANT: Neuhaus, Jean-Marc

APPLICANT: Payne, George B.

APPLICANT: Sperison, Christoph

APPLICANT: Stinson, Jeffrey R.

APPLICANT: Uknes, Scott J.

APPLICANT: Ward, Eric R.

APPLICANT: Williams, Shericea C.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,315

FILING DATE: 24-MAY-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271

FILING DATE: 13-JAN-94

APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566

FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-449-315-103
Alignment Scores:
Pred. No.: 118e-27 Length: 653
Score: 261.00 Matches: 51
Percent Similarity: 62.50% Conservative: 24
Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: 1 Gaps: 0
US-10-005-429-14 (1-126) x US-08-449-315-103 (1-653)
Qy 2 AlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArgMet 21
Db 69 TCATCCGAGGAGGACAAAGTGTTCGGCTGCCACAAAGTTTCGAGGAATGGAACGAGTACTTC 128
Qy 22 AlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCysSer 41
Db 129 AAGAAAGGCGTGTGAGACTAAGAAACCTGGTGTGTGCTGCAITTTACTGCTTCATGTTGGCGGS 188
Qy 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
Db 189 CCTTGGCGTTTATGCCCCCAATCTTCTGACATTCCTAAGAGATGCCCATGTATA 248
Qy 62 PheLeuGluValAspValAspGluLeuLeuGluValAla-LysIleTyrGlyValHisVa 81
Db 249 TTCCTCAAGCTTGATGTGTGATGAACCTGAGACTGTTTCAGCGGAATGGAGTGGAGGC 308
Qy 81 lMetProThrPheCysPheIleArgAenGlyGluThrLeuGluSerPheAlaThrValAs 101

Db 309 AATGCCAACTTTGCTTCATTAAAGATGGAAAGAGTGGACAGAGTTGTTGGTGCCTAA 368
QY 101 pGluaspGluLeuAargspAlaValaLgLyTyAlaAlaLgLyThrThrAla 120
Db 369 GAAAGAGAGTTGACGAGCAGACCATAGTGAAGCATGCTCTCTGCTACTGCTGCT 426

RESULT 4

US-08-444-803-103
; Sequence 103 Application US/08444803
; Patent No. 5654414

GENERAL INFORMATION:

; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Melms, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericea C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,803
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT 1989

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-444-803-103

Alignment Scores:

Pred. No.: 1.18e-27 Length: 653
Score: 261.00 Matches: 51
Percent Similarity: 62.50% Conservative: 24
Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: 1 Gaps: 0

US-10-005-429-14 (1-126) x US-08-444-803-103 (1-653)

QY 2 AlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheaspAlaArgMet 21
Db 69 TCATCCGAGGAGGAGCAAGTGTTCGGCTGCCACCAAGTTGAGGATGGAACGACTTTC 128
QY 22 AlalysAlalysGluGlnGlyLysLeuValValIleaspPheMetAlaProTyrCysSer 41
Db 129 AAGAAAGCGCTTGAGACTAAGAACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 188
QY 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
Db 189 CCTTGGCGTTTATTGCCCCCAATTCCTGCTGACATTGCTAAGAGATGCCCATGTTATA 248
QY 62 PheLeuGluValaspValaspGluLeuLeuGluValAlaLysIleTyrGlyValHisVa 81
Db 249 TTCTCAAGGTTCATGTTGATGAACACTGTTTCAGCGGGAATGAGTGTGGAGGC 308
QY 81 lMetProThrPheCysPheIleAargspGlyGluThrLeuGluSerPheAlaThrValas 101
Db 309 AATGCCAACTTTGCTTCATTAAAGATGGAAAGAGTGGACAGAGTTGTTGGTGCCTAA 368
QY 101 pGluaspGluLeuAargspAlaValaLgLyTyAlaAlaLgLyThrThrAla 120
Db 369 GAAAGAGAGTTGACGAGCAGACCATAGTGAAGCATGCTCTCTGCTACTGCTGCT 426

RESULT 5

US-08-449-043-103
; Sequence 103 Application US/08449043
; Patent No. 5689044
; GENERAL INFORMATION:

APPLICANT: Ryals, John A.
 APPLICANT: Alexander, Danny C.
 APPLICANT: Beck, James J.
 APPLICANT: Duesing, John H.
 APPLICANT: Friedrich, Leslie B.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Harms, Christian
 APPLICANT: Meins, Jr., Frederick
 APPLICANT: Montoya, Alice
 APPLICANT: Moyer, Mary B.
 APPLICANT: Neuhaus, Jean-Marc
 APPLICANT: Payne, George B.
 APPLICANT: Sperison, Christoph
 APPLICANT: Stinson, Jeffrey R.
 APPLICANT: Uknes, Scott J.
 APPLICANT: Ward, Eric R.
 APPLICANT: Williams, Shericca C.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,043
 FILING DATE: 24-MAY-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/181,271
 FILING DATE: 13-JAN-94
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847
 FILING DATE: 6-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,441
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672

FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 653 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-449-043-103
 Alignment Scores:
 Pred. No.: 1.18e-27 Length: 653
 Score: 261.00 Matches: 51
 Percent Similarity: 62.50% Conservative: 24
 Best Local Similarity: 42.50% Mismatches: 44
 Query Match: 40.03% Indels: 1
 DB: 0
 US-10-005-429-14 (1-126) x US-08-449-043-103 (1-653)
 Qy 2 AlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArgMet 21
 Db 69 TCATCCGAGGAGGAGGACAGGTTCGGCTGCCACAGGTTGAGGAATGGAACGAGTACTTC 128
 Qy 22 AlaAlaGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 41
 Db 129 AAGAAAGCGCGTTCAGACTAAGAAACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 189
 Qy 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
 Db 189 CTTGCGCGTTTATGCCCCCAATCTTGTCGACATTGTAAGAAGATGCCCATGTTATA 248
 Qy 62 PheLeuGluValAspValAspGluLeuGluValAla-LysIleTyrGlyValHisVa 81
 Db 249 TTCTCAAGGTTCATGTTCATGAACCTGATGAACCTGATGAACCTGATGAACCTGATGA 308
 Qy 81 lMetProThrPheCysPheIleArgGluGluGluGluGluGluGluGluGluGluGlu 101
 Db 309 AATGCCCACTTTTGTCTTCATTAAAGATGAAAGATGAAAGATGAAAGATGAAAGATG 368
 Qy 101 pGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
 Db 369 GAAAGAGGAGTTCGACGACGACCATAGTAGAAGCATGCTGCTCTACTGTCTACTGCT 426
 RESULT 6
 US-08-456-265A-103
 Sequence 103, Application US/08456265A
 Patent No. 5767369
 GENERAL INFORMATION:
 APPLICANT: Alexander, Danny C.
 APPLICANT: Ryals, John A.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Stinson, Jeffrey R.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 520 White Plains Road, P.O. Box 2005
 CITY: Tarrytown

STATE: New York
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/456,265A
 FILING DATE: 31-MAY-95
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/181,271
 FILING DATE: 13-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847
 FILING DATE: 6-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,441
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Weigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8587
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 653 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-456-265A-103

Alignment Scores:
 Pred. No.: 1.18e-27 Length: 653
 Score: 261.00 Matches: 51
 Percent Similarity: 62.50% Conservative: 24
 Best Local Similarity: 42.50% Mismatches: 44
 Query Match: 40.03% Indels: 1
 DB: Gaps: 0
 US-10-005-429-14 (1-126) x US-08-456-265A-103 (1-653)
 QY 2 AlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArgMet 21
 DB 69 TCATCCGAGGAGGCAAGTTCGGCTGCCAAGTTCGAGGAATGGAACGAGTACTTC 128
 QY 22 AlaAlaLysGluGluGlyLysLeuValIleAspPheMetAlaProTyrCysSer 41
 DB 129 AAGAAAGCGCTTGAGACTAAGAACTGGTGGTGCATTTTACTGCTTCATGGTGGG 188
 QY 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
 DB 189 CTTGCGGTTTATTGCCCCCAATTCCTGACATTCGTAAAGAGATGCCCCCATGTTATA 249
 QY 62 PheLeuGluValAspValAspGluLeuGluValAla-LysIleTyrGlyValHisVa 81
 DB 249 TTCTCAAGGTTGATGTGATGAACCTGAAGACTGTTTCAGCGGAATGGAGTGGAGGC 308
 QY 81 lMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValAs 101
 DB 309 AATGCCAACTTTTGTCTTTCATTAAGATGAAAGAGTGCACAGAGTGTGTGTGCGCAA 368
 QY 101 pGluAspGluLeuArgAspAlaValArgTyrTyrAlaAlaAlaGlyThrThrAla 120
 DB 369 GAAAGAGGNGTTGCAGCAGACCATATGAGGAGCATGCTCTCTCTCTCTCTCTCTCT 426

RESULT 7
 US-08-455-416-103
 Sequence 103, Application US/08455416
 Patent No. 5777200
 GENERAL INFORMATION:
 APPLICANT: Ryals, John A.
 APPLICANT: Alexander, Danny C.
 APPLICANT: Beck, James J.
 APPLICANT: Duesing, John H.
 APPLICANT: Friedrich, Leslie B.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Harms, Christian
 APPLICANT: Meins, Jr., Frederick
 APPLICANT: Montoya, Alice
 APPLICANT: Meyer, Mary B.
 APPLICANT: Neuhaus, Jean-Marc
 APPLICANT: Payne, George B.
 APPLICANT: Sperison, Christoph
 APPLICANT: Stinson, Jeffrey R.
 APPLICANT: Uknes, Scott J.
 APPLICANT: Ward, Eric R.
 APPLICANT: Williams, Shericca C.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,416

APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/358,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
NAME: Elmer, James Scott
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8699
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-455-244-103

Alignment Scores:
Pred. No.: Length: 653
Score: 261.00 Matches: 51
Percent Similarity: 62.50% Conservative: 24
Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: 1 Gaps: 0

US-10-005-429-14 (1-126) x US-08-455-244-103 (1-653)

QY 2 AlaAlaGluGluValAlaValAlaCysHisThrLysAspGluPheAspAlaArgMet 21
Db 69 TCATCGAGAGGAGGACAGTGTTCGCTCCACAGTTGAGGATGGACGAGTACTTC 128
QY 22 AlaLysAlaLysGluGlnGlyLysLeuValValLeuValAlaAspPheMetAlaProTrpCysSer 41
Db 129 AAGAAAGGCGTTCAGACTAAGAACTGGTGTGCTGCAATTTACTGCTTCATGTCGCGS 188
QY 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
Db 189 CTTGGCGGTTTATTGCCCCCAATTCTGTGACATTGCTGAAGAGATGCCCATGTATA 248

QY 62 PheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHisVa 81
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QY 81 lMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValAs 101
Db 309 AATGCCAACTTTTCTCTTCATTAAAGATGAAAAGAGTGGACAGAGCTTGTGGTGCAA 368
QY 101 pGluAspGluLeuArgAspAlaValAlaArgLysTyrAlaAlaAlaGlyThrThrAla 120
Db 369 GAAAGAGGAGTTGCAGCAGACCATAGTGAAGCATGCTCTCTCTGCTACTGTCTACTGT 426
RESULT 9
US-08-454-876-103
Sequence 103, Application US/08454876
Patent No. 5804593
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993

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PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/632,441
  FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/425,504
  FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/848,506
  FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/768,122
  FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/580,431
  FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/368,672
  FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/329,018
  FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/045,957
  FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
  NAME: Elmer, James Scott
  REGISTRATION NUMBER: 36,129
  REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
  TELEPHONE: (919)541-8614
  TELEFAX: (919)541-8689
  INFORMATION FOR SEQ ID NO: 103:
    LENGTH: 653 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
US-08-454-876-103

Alignment Scores:
Pred. No.: 1,18e-27 Length: 653
Score: 261.00 Matches: 51
Percent Similarity: 62.50% Conservative: 24
Best Local Similarity: 42.50% Mismatches: 44
Query Match: 40.03% Indels: 1
DB: Gaps: 0

US-10-005-429-14 (1-126) x US-08-454-876-103 (1-653)
Qy 2 AlaAlaGluGluGluValAlaValAlaCysHisThrLysAspGluPheAspAlaArgMet 21
Db 69 TCAATCCGAGGAGGACGACGAGTTCGCTGCCACACAGGTTGAGGATGGACGAGTACTTC 128
Qy 22 AlaAlaLysGluGluGluGluValAlaValAlaAspPheMetAlaProThrCysSer 41
Db 129 AAGAAAGGGCGTTGAGACTAAGAACTGGTGGTGCATTTACTGCTTCATGTCGCGS 188
Qy 42 GlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAlaVal 61
Db 189 CCTTGGCGTTTATGCCCCCAATTCCTGCACTGCTAAGAGATGCCCATGTTATA 248
Qy 62 PheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHisVa 81
Db 249 TTCTCAAGGTTCATGTTGATGAACCTGAACACTGTTTCACGGCGGAATGGAGTGGAGGC 308
Qy 81 lMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrValAs 101
Db 309 AATGCCCAACTTTTGTCTCTTCATTAAAGATGAAAGAGTGGACAGAGTGTGTCGCCAA 368
Qy 101 pGluAspGluLeuArgAspAlaValAlaGlyTyrAlaAlaGlyThrThrAla 120
Db 369 GAAAGAGCACTTGCAGCAGACCATAGTGAAGCATGCTGCTCTCTGCTACTGCTACTGCT 426
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RESULT 10

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US-08-457-364-103
  Sequence 103, Application US/08457364
  Patent No. 5847258
  GENERAL INFORMATION:
    APPLICANT: Ryals, John A.
    APPLICANT: Alexander, Danny C.
    APPLICANT: Beck, James J.
    APPLICANT: Duesing, John H.
    APPLICANT: Friedrich, Leslie B.
    APPLICANT: Goodman, Robert M.
    APPLICANT: Harms, Christian
    APPLICANT: Meins, Jr., Frederick
    APPLICANT: Montoya, Alice
    APPLICANT: Moyer, Mary B.
    APPLICANT: Neuhaus, Jean-Marc
    APPLICANT: Payne, George B.
    APPLICANT: Sperison, Christoph
    APPLICANT: Stinson, Jeffrey R.
    APPLICANT: Unnes, Scott J.
    APPLICANT: Ward, Eric R.
    APPLICANT: Williams, Shericca C.
  TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
  TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
  NUMBER OF SEQUENCES: 106
  CORRESPONDENCE ADDRESS:
    ADDRESSER: CIBA-GEIGY Corporation
    STREET: 7 Skyline Drive
    CITY: Hawthorne
    STATE: New York
    COUNTRY: USA
    ZIP: 10532
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patent In Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/457,364
      FILING DATE: 31-MAY-1995
      CLASSIFICATION: 800
    PRIOR APPLICATION DATA:
      PRIOR APPLICATION NUMBER: 08/181,271
      FILING DATE: 13-JAN-94
      APPLICATION NUMBER: US 08/093,301
      FILING DATE: 16-JUL-1993
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/937,197
        FILING DATE: 6-NOV-1992
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/678,378
        FILING DATE: 1-APR-1991
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/305,566
        FILING DATE: 6-FEB-1989
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/165,667
        FILING DATE: 8-MAR-1988
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/042,847
        FILING DATE: 6-APR-1993
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/632,441
        FILING DATE: 21-DEC-1990
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/425,504
        FILING DATE: 20-OCT-1989
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/848,506
        FILING DATE: 6-MAR-1992
      APPLICATION NUMBER: US 07/768,122
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1  APPLICATION NUMBER:  US 08/045,957
2
3  FILING DATE:  12-APR-1993
4  ATTORNEY/AGENT INFORMATION:
5  NAME:  Elmer, James Scott
6  REGISTRATION NUMBER:  36,129
7  REFERENCE/DOCKET NUMBER:  S-19825/P1/CGC 1727
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE:  (919)541-8614
10 TELEFAX:  (919)541-8689
11 INFORMATION FOR SEQ ID NO:  103:
12 SEQUENCE CHARACTERISTICS:
13     LENGTH:  653 base pairs
14     TYPE:  nucleic acid
15     STRANDEDNESS:  single
16     TOPOLOGY:  linear
17     MOLECULE TYPE:  DNA (genomic)
18 US-08-456-262-103

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Alignment Scores:		
Pred. No.:	1.18e-27	653
Score:	261.00	51
Percent Similarity:	62.50%	Conservative: 24
Best Local Similarity:	42.50%	Mismatches: 44
Query Match:	40.03%	Indels: 1
DB:	2	Gaps: 0

US-10-005-429-14 [1-126] x US-08-456-262-103 (1-653)

QY	2	AlaalaGluGluGluAlaValIlleAlaCysHisThrLysAspGluPheAspAlaArgMet	21
Db	69	TCATCCAGGAGGACAAAGTGTTCGGGTGCCACAAGGTGTGAGGAATGGAACCGTACTTC	128
QY	22	AlaLysAlaLysGluGluGlyLysLeuValValIleAspPheMetAlaProTyrCysSer	41
Db	129	ARGNAAGCGTTGAGACTAAGAAACTGTTGGTGTGGATTACTGCTTCATGGTGGCGS	188
QY	42	GlyCysGlnMetMetAlaProValTyrAlaAlaAspCysAlaSerLysTyrProSerAlaVal	61
Db	189	CCTTGCCTGTTTATTTGCCCAATCTTCTGCACATGCTAAGAAGATCCCCATGTTATA	248
QY	62	PheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyIValHisVala	81
Db	249	TTCTCTCAAGGTTGATGTGATGAAGACTGTTTCAGCGGGAATGGAGTGTGGAGGC	308
QY	81	LmetProThrPheCysPheIleArgAsnGlyCluThrLeuGluSerPheAlaThrValAs	101
Db	309	AATGCCAACTTTGTTCTTCATTTAAAGATGGAAAGAGAGTGGTGTGGTGCCAA	368
QY	101	pGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla	120
Db	169	GAAGAGGAGGTTTGGAGGACACCACTCAAGCATCTCTCTCTGCTACTGTCACTGCT	426

RESULT 12

RESOL 12
US-08-456-240-103
: Sequence 103. Application US/08456240

Sequence 103, Applica
Patent No. 5856154
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.

Db 249 TTCTCAAGGTGATGTTGATGAAGTGTTCGCGGAGTGGAGGTC 308
Qy 81 lMetProthrPheCysPheIleArgAsnGlyThrLeuGluSerPheAlaThrValas 101
Db 309 AATGCCAATTTTGTCTTCAATTAAGATGGAAGAGTGGACAGAGTTGTGTGCGCAA 368
Qy 101 pGluaspGluLeuArgAspAlaValaArgGlyTyraAlaAlaGlyThrThrAla 120
Db 369 GAAAGAGGAGTGGACAGACCATAGTGAAGCATGCTCTCTCTACTGTCTACTGCT 426

RESULT 15
US-09-350-600-103
Sequence 103, Application US/09350600
Patent No. 6262342
GENERAL INFORMATION:
APPLICANT: Meins, Frederick
APPLICANT: Shinshi, Hideaki
APPLICANT: Wenzler, Herman
APPLICANT: Hofsteenge, Jan
APPLICANT: Ryals, John
APPLICANT: Sperisen, Christoph
TITLE OF INVENTION: DNA SEQUENCES ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING BETA-1,3-GLUCANASE ACTIVITY
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6262342artis Corporation
STREET: 3054 Cornwallis Road, P.O. Box 12257
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatenIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,600
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/971,217
FILING DATE: 14-NOV-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/457,364
FILING DATE: 31-MAY-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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FILING DATE: 24-MAR-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/381,443
FILING DATE: 18-JUL-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/353,312
FILING DATE: 17-MAY-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/226,303
FILING DATE: 29-JUL-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-198250
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-350-600-103

Alignment Scores:
Pred. No.: 1.18e-27
Score: 261.00
Percent Similarity: 62.50%
Best Local Similarity: 42.50%
Query Match: 40.03%
DB: 3
Gaps: 0
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Qy 2 AlaAlaGluGluGlyAlaValAlaIleAlaCysHisThrIysAspGluPheAspAlaArgMet 21
Db 69 TCATCCGAGGAGGAGCAAGTGTTCGGCTGCCACCAAGTTGAGGAGTGAAGAGTACTTC 128
Qy 22 AlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProTrpCysSer 41
Db 129 AAGAAAGCGGTTGAGACTAAGAACTGGTGTGTGCTGCTTTACTGCTTCTGTCGCGS 188
Qy 42 GlyCysGlnMetAlaProValTyAlaAspCysAlaSerIysTyProSerAlaVal 61
Db 189 CTTGCGCGTTTTATTGCCCCCAATTTCTGTGACATTCGTAAGAAGATGCCCATGTTATA 248
Qy 62 PheLeuGluValAspValAspGluLeuValAlaLysIleTyGlyValHisVa 81
Db 249 TTCTCAAGGTGATGTTGATGAAGTGTTCGCGGAGTGGAGGTC 308
Qy 81 lMetProthrPheCysPheIleArgAsnGlyThrLeuGluSerPheAlaThrValas 101
Db 309 AATGCCAATTTTGTCTTCAATTAAGATGGAAGAGTGGACAGAGTTGTGTGCGCAA 368

QY 101 pGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla 120
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	633	97.1	780	13	US-10-425-114-17100	Sequence 17100, Ap
5	361	55.4	540	15	US-10-349-782-12	Sequence 12, Appl
6	355.5	54.5	684	13	US-10-425-114-26038	Sequence 26038, A
7	342	52.5	596	13	US-10-425-114-23491	Sequence 23491, A
8	339	52.0	548	13	US-10-425-114-23500	Sequence 23500, A
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14	338	51.8	594	13	US-10-425-114-17618	Sequence 17618, A
15	338	51.8	692	13	US-10-425-114-23337	Sequence 23337, A
16	338	51.8	739	13	US-10-425-114-21079	Sequence 21079, A
17	338	51.8	835	13	US-10-425-114-27303	Sequence 27303, A
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19	335	51.4	577	13	US-10-425-114-6528	Sequence 6528, Ap
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23	338	50.3	699	16	US-10-260-238-180	Sequence 180, App
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25	305.5	46.9	360	9	US-09-938-842A-164	Sequence 164, App
26	305.5	46.9	360	11	US-09-938-842A-164	Sequence 164, App
27	285	43.7	3888	9	US-09-897-898-10	Sequence 10, Appl
28	285	43.7	3888	13	US-09-897-898-10	Sequence 45, Appl
29	285	43.7	3888	15	US-10-032-201B-19	Sequence 19, Appl
30	282	43.3	345	9	US-09-938-842A-163	Sequence 163, App
31	282	43.3	345	11	US-09-938-842A-163	Sequence 163, App
32	282	43.3	345	15	US-10-032-201B-38	Sequence 38, Appl
33	282	43.3	1339	13	US-10-290-072-209	Sequence 209, App
34	282	43.3	1344	13	US-10-290-072-238	Sequence 238, App
35	282	43.3	1345	13	US-10-290-072-213	Sequence 213, App
36	282	43.3	1345	13	US-10-290-072-215	Sequence 215, App
37	282	43.3	1348	13	US-10-290-072-211	Sequence 211, App
38	282	43.3	3129	9	US-09-897-898-5	Sequence 5, Appli
39	282	43.3	3129	13	US-09-897-898-5	Sequence 40, Appl
40	282	43.3	3129	15	US-10-032-201B-14	Sequence 14, Appl
41	282	43.3	3888	9	US-09-897-898-7	Sequence 7, Appli
42	282	43.3	3888	13	US-09-897-898-7	Sequence 42, Appl
43	282	43.3	3888	15	US-10-032-201B-16	Sequence 16, Appl
44	275	42.2	851	13	US-10-424-599-47701	Sequence 47701, A
45	275	42.2	4935	15	US-10-032-201B-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-10-425-114-16798
; Sequence 16798, Application US/10425114

; Publication No. US2004003488A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E.

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 16798

; LENGTH: 731

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3067-008-E2_FLI

US-10-425-114-16798

Alignment Scores:
Pred. No.: 1.37e-87 Length: 731
Score: 652.00 Matches: 126
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-005-429-14 (1-126) x US-10-425-114-16798 (1-731)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 49 ATGGCGCGGAGAGGGTGGCGTGTATCGCTGCCACACAGGAGAGTTCAGCCCGC 108
Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 109 ATGGCCAAAGCCCAAGGAGCAGGCAAGCTGTGGTTCATCGACTTCATGGCCCGCTGGTGC 168
Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db 169 ACTGGGTGTCAGATGATGCGCCCGGTGTACGGGACTGCGCAGCAAGTACCTTCCCGC 228
Qy 61 ValPheLeuGluValAspValAspGluLeuValAlaLysIleTyrGlyValHis 80
Db 229 GTCTTCCTCGAGTTCAGCTCGACGACTGCTGGAGTTCGGAAGTCTACGGCGTCCAT 288
Qy 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db 289 GTGATGCGCGACCTTCTGCTTTCATCAGGAACGGCGAGAGCTCGAGAGCTTTCGCTACCGTC 348
Qy 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
Db 349 GACGAGGAGAGCTCCGGAGCGCGTTCAGAGAGTACCGCCCGCTGGCACTACGACGAGCT 408
Qy 121 ProAlaSerAlaSerAla 126
Db 409 CTGCTCGCGGCTCGGCC 426

RESULT 2

US-10-425-114-16904
; Sequence 16904, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingsong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 16904
; LENGTH: 742
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3067-031-H6_FLI
; US-10-425-114-16904

Alignment Scores:
Pred. No.: 1.4e-87 Length: 742
Score: 652.00 Matches: 126
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-005-429-14 (1-126) x US-10-425-114-16904 (1-742)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 46 ATGGCGCGGAGAGGGTGGCGTGTATCGCTGCCACACAGGAGAGTTCAGCCCGC 105
Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 106 ATGGCCAAAGCCCAAGGAGCAGGCAAGCTGTGGTTCATCGACTTCATGGCCCGCTGGTGC 165
Qy 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
Db 166 AGTGGGTGCGCAGATGATGCGCCCGGTGTACGGGACTGCGCAGCAAGTACCTTCCCGC 225
Qy 61 ValPheLeuGluValAspValAspGluLeuValAlaLysIleTyrGlyValHis 80
Db 226 GTCTTCCTCGAGTTCAGCTCGACGACTGCTGGAGTTCGGAAGTCTACGGCGTCCAT 285
Qy 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
Db 286 GTGATGCGCGACCTTCTGCTTTCATCAGGAACGGCGAGAGCTTCGAGAGCTTTCGCTACCGTC 345
Qy 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaGlyThrThrAla 120
Db 346 GACGAGGAGAGCTCCGGAGCGCGTTCAGGAGTACCGCCCGCTGGCACTACGACGAGCT 405
Qy 121 ProAlaSerAlaSerAla 126
Db 406 CTGCTCGCGGCTCGGCC 423

RESULT 3

US-10-425-114-17028
; Sequence 17028, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingsong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 17028
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3067-048-H2_FLI
; US-10-425-114-17028

Alignment Scores:
Pred. No.: 1.43e-87 Length: 752
Score: 652.00 Matches: 126
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-005-429-14 (1-126) x US-10-425-114-17028 (1-752)

Qy 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
Db 56 ATGGCGCGGAGAGGGTGGCGTGTATCGCTGCCACACAGGAGAGTTCAGCCCGC 115
Qy 21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTyrCys 40
Db 116 ATGGCCAAAGCCCAAGGAGCAGGCAAGCTGTGGTTCATCGACTTCATGGCCCGCTGGTGC 175

Qy	41	SerGlyCysGlnMetSerAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla	60
Db	176	AGTGGTGTGCACATGATGATGCCCGGTGTACGCGACTGCGCCAGCAAGTACCCGCGG	235
Qy	61	ValPheLeuGluValAspValAspGluLeuLeuGluValAlaLysIleTyrGlyValHis	80
Db	236	GTCCTTCCTCGAGTCCAGTGTGCAGCACTGCTGGAGTCCGAGAGATCTACGGCGTCCAT	295
Qy	81	ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal	100
Db	296	GTGATGCCGACCTTCTGTCTCATCAGGAACGGCGAGACGCTTCGAGAGCTTTGTCTACCGTC	355
Qy	101	AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla	120
Db	356	GACGAGGACGAGCTCCGGAGCGCTCAGGAAGTACCGCGCGCTGCGACTACGACGGCT	415
Qy	121	ProAlaSerAlaSerAla	126
Db	416	CCTGGCTGGCGGTCCGCC	433

RESULT 4

```

US-10-425-114-7100
; Sequence 7100, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7100
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700617241_FLI
US-10-425-114-7100

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Db      342  GTGATGCCGACCTTCTGCTTCATCAGGNAACGGCGAGAGCGCTCGAGAGCTTTGCTACCGTC 401
Qy      101  AspcLuaspGluLeuAgaSPAlaValArgIysTyr-----AlaAlaAlaGlyThrThr 118
Db      402  GACGAGACGAGCTCCGGAACGCGCTCAGGAAGTACGCGCGCGCGCGCGCGCACTACG 461
Qy      119  ThrAlaProAlaSerAlaSerAla 126
Db      462  ACGGCTCTCGCTCGGCGTCCGCC 485

RESULT 5
US-10-349-782-12
; Sequence 12, Application US/10349782
; Publication No. US20030143618A1
; GENERAL INFORMATION:
; APPLICANT: Yves Hatzfield
; APPLICANT: Valerie Marie-No. US20030143618A1lle Frankard
; APPLICANT: Anne-Marie Droual
; TITLE OF INVENTION: Method for easy cloning and selection of chimeric DNA molecules
; FILE REFERENCE: 1187-15
; CURRENT APPLICATION NUMBER: US/10/349,782
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: EP 02075373.7
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 540
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified thioredoxin of Oryza sativa in vector pDONR201
US-10-349-782-12

Alignment Scores:
Pred. No.: 3,72e-44 Length: 540
Score: 361.00 Matches: 70
Percent Similarity: 71.77% Conservative: 19
Best Local Similarity: 56.45% Mismatches: 33
Query Match: 55.37% Indels: 2
DB: 15 Gaps: 1

US-10-005-429-14 (1-126) x US-10-349-782-12 (1-540)

```

RESULT 6


```
US-10-425-114-26038
; Sequence 26038, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 23491
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3596-054-E10_FLI
US-10-425-114-23491
Alignment Scores:
Pred. No.: 3,02e-41 Length: 596
Score: 342.00 Matches: 65
Percent Similarity: 70.00% Conservative: 19
Best Local Similarity: 54.17% Mismatches: 36
Query Match: 52.45% Indels: 0
DB: 13 Gaps: 0
US-10-005-429-14 (1-126) x US-10-425-114-23491 (1-596)
QY 1 MetAlaAlaGluGluGlyAlaValAlaCysHisThrLysAspGluPheAspAlaArg 20
DB 65 ATGGGTCGCGAGGAGGAGTCTGTCATCGCTCCCTGCCACACCAAGGCGCGACTTCGACGCCAC 124
QY 21 MetAlaLysAlaLysGluGlnGlyValValLysValValLysPheMetAlaProTyrCys 40
DB 125 ATGCCCAAGGCCAAGGAGGCGGCAAGCTGGTGATCTTGAATCTTCAACGCGCTCTCTGCTGC 184
QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
DB 185 GGCCCTCGCGCTTCATCGCGCCACTGTTCGTGCGACGACGCAAGAGTTCAACCCAGGCT 244
QY 61 ValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHis 80
DB 245 GTGTTCTCTGAAGGTGGACGTCGACGAGCTGAAGGAGTTCGCGGCGCTCTACGATGTCGAG 304
QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
DB 305 CGCATCGCGACTTCCTCCACTTCGTCAAGACGCGGTGACGGTGGAGACCGTCTCGGTGCC 364
QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGlyThrThrAla 120
DB 365 AGGAAGGAGACCTCTCTGCGCCCGATCGAAGACACTCGCGCGCGCGCTGTCTGCTCGC 424
RESULT 8
US-10-425-114-23500
; Sequence 23500, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 23500
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3596-057-G4_FLI
US-10-425-114-23500
```

```
US-10-425-114-26038
; Sequence 26038, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26038
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4073-004-E6_FLI
US-10-425-114-26038
Alignment Scores:
Pred. No.: 3.5e-43 Length: 684
Score: 355.50 Matches: 72
Percent Similarity: 69.70% Conservative: 20
Best Local Similarity: 54.55% Mismatches: 33
Query Match: 54.52% Indels: 7
DB: 13 Gaps: 1
US-10-005-429-14 (1-126) x US-10-425-114-26038 (1-684)
QY 1 MetAlaAlaGluGluGlyAlaValAlaCysHisThrLysAspGluPheAspAlaArg 20
DB 93 ATGGGTCGCGAGGAGGAGTCTGTCATCGCTGCCACCAAGGCGCGACTTCGACGCCAC 152
QY 21 MetAlaLysAlaLysGluGlnGlyValValLysValValLysPheMetAlaProTyrCys 40
DB 153 ATGCCAAGGCCAAGGAGGCGCGAGCTGGTGATCTTGAATCTTCAACGCGCTCTCTGCTGC 212
QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
DB 213 GGTCTCTGCGCGCCATCGCTCCACTGTGTCGAGCAGCGCAAGAGTACACTCAAGCT 272
QY 61 ValPheLeuGluValAspValAspGluLeuGluValAlaLysIleTyrGlyValHis 80
DB 273 GTCTTCTCTGAAGGTGGACGTCGACGAGCTGAAGGAGTTACTCGACGATCAAGATCGAG 332
QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
DB 333 CGCATCGCGACTTCCTCCACTTCATCAAGAACGCGGAGCGGTGAGACTATCGTCTGCTGCC 392
QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaAlaAlaGly----- 116
DB 393 AGGAAGGAGACGCTCTCTGCGCCCTGTATCTCAAGAGCATACCGCGTCTGCTCGCGGTAAAGAA 452
QY 117 -----ThrThrAlaProAlaSerAlaSer 125
DB 453 GATAGTCAGTCGTCGTCATATAGGGCCAGCGCATCG 488
RESULT 7
US-10-425-114-23491
; Sequence 23491, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
```


Db 176 GGTCCATGCCGCGCCATCGCCCACTGTTCTGCGAACACGCCAAGAGTTCACTCAGGTC 235
 QY 61 ValPheLeuGluValAspValAspGluLeuLeuValAlaLysIleTyrGlyValHis 80
 Db 236 GTCTTCTTGAAGTGGAGCTGCGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 295
 QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 Db 296 GCGATGCCGAGCTTCCACTTGTCAAGAACGGCAAGAGCTGCGACCATCGTGGTGCC 355
 QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaLysIleThrThrAla 120
 Db 356 AAGAAGGACGAGCTCTCTGGCCCTGATCGAAGCATCGCGC-----CCTGGC 403
 QY 121 ProAlaSerAlaSerAla 126
 Db 404 CCTGGCTCTGGCTCTGCC 421

RESULT 11

US-10-260-238-5754
 ; Sequence 5754, Application US/10260238
 ; Publication No. US20040016025A1

GENERAL INFORMATION:

; APPLICANT: Budworth, Paul R.
 ; APPLICANT: Moughamer, Todd G.
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiyaki
 ; APPLICANT: Krieps, Joel
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Ricke, Darrell
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
 ; FILE REFERENCE: 60111-NP
 ; CURRENT APPLICATION NUMBER: US/10/260,238
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,448
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; NUMBER OF SEQ ID NOS: 6077
 ; SEQ ID NO 5754
 ; LENGTH: 366
 ; TYPE: DNA
 ; ORGANISM: Zea mays

US-10-260-238-5754

Alignment Scores:
 Pred. No.: 5,92e-41 Length: 366
 Score: 338.00 Matches: 67
 Percent Similarity: 69.05% Conservative: 20
 Best Local Similarity: 53.17% Mismatches: 35
 Query Match: 51.84% Indels: 4
 DB: 16 Gaps: 1

US-10-005-429-14 (1-126) x US-10-260-238-5754 (1-366)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 Db 1 ATGGCGTCCGAGCAGGAGTGTGATCGGTGCCACAGCAGAGGCTGAGTTCCAGCCCCAC 60
 QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProThrCys 40
 Db 61 ATGACCAAGGCCCGCAGGAAGCCGCAAGCTGGTGGTTCATCGACTTCACTCCGCCCTGGTGC 120
 QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
 Db 121 GGTCCATGCCGCGCCATCGCCCACTGTTCTGCGAACACGCCAAGAGTTCACTCAGGTC 180

QY 61 ValPheLeuGluValAspValAspGluLeuLeuValAlaLysIleTyrGlyValHis 80
 Db 181 GTCTTCTTGAAGTGGAGCTGCGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 240
 QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 Db 241 GCGATGCCGAGCTTCCACTTGTCAAGAACGGCAAGAGCTGCGACCATCGTGGTGCC 300
 QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaLysIleThrThrAla 120
 Db 301 AAGAAGGACGAGCTCTCTGGCCCTGATCGAAGCATCGCGC-----CCTGGC 348
 QY 121 ProAlaSerAlaSerAla 126
 Db 349 CCTGGCTCTGGCTCTGCC 366

RESULT 12

US-10-425-114-35628
 ; Sequence 35628, Application US/10425114
 ; Publication No. US20040034888A1

GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yibua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 35628
 ; LENGTH: 565
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-ZMROB73071012_FLI
 US-10-425-114-35628

Alignment Scores:

Pred. No.: 1.11e-40 Length: 565
 Score: 338.00 Matches: 67
 Percent Similarity: 69.05% Conservative: 20
 Best Local Similarity: 53.17% Mismatches: 35
 Query Match: 51.84% Indels: 4
 DB: 13 Gaps: 1

US-10-005-429-14 (1-126) x US-10-425-114-35628 (1-565)

QY 1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
 Db 35 ATGGCGTCCGAGCAGGAGTGTGATCGGTGCCACAGCAGAGGCTGAGTTCCAGCCCCAC 94
 QY 21 MetAlaLysAlaLysGluGlnGlyLysLeuValValIleAspPheMetAlaProThrCys 40
 Db 95 ATGACCAAGGCCCGCAGGAAGCCGCAAGCTGGTGGTTCATCGACTTCACTCCGCCCTGGTGC 154
 QY 41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLysTyrProSerAla 60
 Db 155 GGTCCATGCCGCGCCATCGCCCACTGTTCTGCGAACACGCCAAGAGTTCACTCAGGTC 214
 QY 61 ValPheLeuGluValAspValAspGluLeuLeuValAlaLysIleTyrGlyValHis 80
 Db 215 GTCTTCTTGAAGTGGAGCTGCGAAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 274
 QY 81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGluSerPheAlaThrVal 100
 Db 275 GCGATGCCGAGCTTCCACTTGTCAAGAACGGCAAGAGCTGGTGGTTCATCGACTTCACTCCGCCCTGGTGC 334
 QY 101 AspGluAspGluLeuArgAspAlaValArgLysTyrAlaLysIleThrThrAla 120

Db 335 AGGAGGACGAGCTCTCTGCGCCAGATCGACGATGCCGCG-----CTTGGC 382

QY 121 ProAlaSerAlaSerAla 126
|||||

Db 383 CCTGGCTCTGGCTTGCC 400
|||||

RESIST 13

```

US-10-425-114-284
; Sequence 284, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)9
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 284
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700052149_FLI
US-10-425-114-284

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Alignment Scores:	
Pred. No.:	1.16e-40
Score:	338.00
Percent Similarity:	39.05%
Best Local Similarity:	53.17%
Query Match:	51.64%
DE:	13
Length:	583
Matches:	67
Conservative:	35
Mismatches:	20
Indels:	4
Gaps:	1

US-10-005-429-14 (1-126) x US-10-425-114-284 (1-583)

[illegible]

41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLvsTyrproSerAla 60

db 167 GGTCCATGCCGCGCCATCGCCCCAATGGTTGGTCTGAACAACGCCAAGAGATTCACTCAGGTC 226

61 valpheLeuGluValAspValAspGluLeuGluValAlaIysIleTyrGlyValHis 80

Db 227 GTCTTCCTGAAGGTGGA CGTGGG CCAAGTCAAGGAAGTCA CCGCGGCTA CCAAGTCCAG 286

81 ValMetProThrPheCysPheIleArgAsnGlyGluThrLeuGlySerPheAlaThrVal 100

D_b 287 GCGATGCCGACCTTCCAATTTCGTCAAGAACGGCAAGACGGTGGCAACATCTGTGGTGCC 346

101 AspGluAspGluLeuArgAspAlaValArgIysTyrAlaAlaIaGlvThrThrAla 120

347 A GGAAGGACGAGCTCCTGGCCAGATCGAGAAAGCATGCCGGG-----CGTGGG 394

121 proAlaserAlaserAla 126

db
395 CCTGGGCTCTGGGTCAGCC 412

RESULT 14

US-10-425-114-17618
; Sequence 17618, Application US/10425114
; Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yanyang

```

1  TITLE OF INVENTION: Nucleic Acid Molecules and Other Structures Associated With
2  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
3  FILE REFERENCE: 38-21 (53313)B
4  CURRENT APPLICATION NUMBER: US/10/425,114
5  CURRENT FILING DATE: 2003-04-28
6  NUMBER OF SEQ ID NOS: 73128
7  SEQ ID NO 17618
8  LENGTH: 594
9  TYPE: DNA
10 ORGANISM: Zea mays
11 FEATURE:
12 OTHER INFORMATION: Clone ID: LIB3070-001-G9_FLI
13 US-10-425-114-17618

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Alignment Scores:	
Pred. No.:	1.2e-40
Score:	338.00
Percent Similarity:	69.05%
Local Similarity:	53.17%
Query Match:	51.84%
DB:	13
Gaps:	1
Length:	594
Matches:	67
Conservative:	20
Mismatches:	35
Indels:	1

US-10-005-429-14 (1-126) x US-10-425-114-17618 (1-594)

1 MetAlaAlaGluGluGlyAlaValIleAlaCysHisThrLysAspGluPheAspAlaArg 20
58 ATGGCTCGCAGCAGGAGTCGTGATCGCGTCCACAGCAGGCTGAGTTGAGCCGAC 117
21 MetAlaLysAlaLysGluGlnGlyLysLeuValIleAspPheMetAlaProTrpCys 40
118 ATGACCAAGGCCGAGAGCCGGCAGCTGTGGTGCATCGACTTCACGCGCCCTGGTGC 177

41 SerGlyCysGlnMetMetAlaProValTyrAlaAspCysAlaSerLvsTyrProSerAla 60

178 GGTCCATGCCCGGCCCATCGCCCCCATGTGTTGGTGGAAACA CGCCAAGAGATTCACTCAGGTC 237

61 val phe leu glu val asp val asp glu leu leu glu val ala val ile tyr gly val his 80

238 GTCTTCCTGAAGGTGGA CGTGGG CCAA GTGA AGGA GTCA CCGGGCCTACGAGGTCGAG 297

81 ValMetProThrPheCysPheTLeArgAsnGlyGluThrIleGluGlnSerPheAlaThrVal100

298 GCGATGCGGACGTTTCAAGTTCTCAAGAAAGCAAGGTCGAGACCATTCGGGGAC 357

101 AsnGluAsnGluLeuArgAsnAlaValArgIstyrAlaAlaIstyrThrThrAla 120

358 AGGAAGGACGAGTCCTGGCCCGATGAGAGCATGCCGGG-----CGTCAG 405

121 PROJ[ASERA]ASERA]a 126

b6
b7C

406 CMTCCCTGCGTCTGC A23

RESIST 15

US-10-425-114-2333)
Sequence 23337 Application US/10425114

PUBLICATION NO. US20040034888A1
GENERAL INFORMATION:

APPLICANT: LIU, Jingdong
APPLICANT: Zhou yibin

APPLICANT: KOVALIC, David K.
APPLICANT: Screen Steven E.

APPLICA
APPLICA

APPLICANT: Cao, Longwei
TITLE OF INVENTION: Nucleic Acid Molec
TITLE OF INVENTION: Plants and Uses Th
FILE REFERENCE: 38-21(53113)B

APPLICANT: Cao, Tongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B

US-10-005-429-14 (1-126) X US-10-425-114-23337 (1-692)

Search completed: May 5, 2004, 08:36:29
Job time : 184.319 secs

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Qy 207 LysileLysValLeuTrpAspSerGluValValGluAlaTyrglyAlaAsnGlyGly 226
Db 625 AAGATTGATGATTGGAACCTCTCTGTTGGAGAGCTTATGGAGATGAGAGAGAT 694
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 685 GTGCTTGGAGATTGAAGTGAAGATGTGTACCGAGATGTTTCTGATTTAAAGTT 744
Qy 247 SerGlyLeuPheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
Db 745 TCTGGATTGTTCTTGTCTATGTTGTCATGAGCCAGCTACCAAGTTTGGATGTTGTT 804
Qy 267 GluLeuAspSerAspGlyTyrrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 805 GAGTTAGATTGGAGTGTATGTTGTCAGAGCTGTGTTATAGGCAAGCATCACTGCTGCA 864
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysTyrrArgGlnAlaIleThrAlaAla 306
Db 865 GGAGTTTTCGCTGGGTGATGTTTCAGGATAAGAGTATAGGCAAGCATCACTGCTGCA 924
Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrrLeuGlnGluIleGlyAlaGln 326
Db 925 GGAACCTGGTGCATGGCAGCTTGGATGCGAGCATTTACTTACAGAGATTGGATCTCAG 984
Qy 327 GluGlyLysSerAsp 331
Db 985 CAAGTAAAGATGAT 999

RESULT 15
US-10-290-072-238
; Sequence 238, Application US/10290072
; Publication No. US20030211511A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Daima, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Luginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 10/141,531
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/285,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 238
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-290-072-238

Alignment Scores:
Pred. No.: 7,79e-160 Length: 1344
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservative: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 4
DB: 13 Gaps: 1

US-10-005-429-25 (1-331) x US-10-290-072-238 (1-1344)

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Search completed: May 5, 2004, 08:36:40
Job time : 463.681 secs

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Db 25 ACAAGCTCTGTATAGAGTGGCCAGCGCCACACACGCGCGGCGATTACGCGAGCT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
Db 85 AGGGCTGAACCTTAACCTCTCTTCGAGAGGATGGATGCTAACGACATCGCTCCCGGT 144
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 145 GGTCACTAACACACCGAGCTGCGAGATTTCCCGGNTTCCAGAGGTATTC 204
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 205 CGAGTAGAGCTCACTGACCAATTCCTTAACATCGAGCGATTCGGTACTACGATATT 264
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysPropheArgValSerAlaAspSer 110
Db 265 ACHAGACGCTGACGAAGTCTGATTTCTTCGAACCGTTTAAGCTATTCACAGATTCA 324
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgLeuHis 130
Db 325 AAAGCCATTCTCGCTGACGCTGTGATTCGCTACTGAGCTGTGGCTGCGTACGCTTAGC 384
Qy 131 Phe-----ProGlySerAspAlaTyTrpAsnArgGlyIleSerAlaCysAla 146
Db 385 TTCGTTGGATCTGGTGAAGTCTCGAGGTTTCTCGAACCGTGAATCTCCGCTTGTGCT 444
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 445 GTTTGCGAGGAGCTCTCCGATATTCGTTACCAAACTCTTCGCGTGTGATCGGTGAGGC 504
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyTrpAsnArgGlyIleLeu 186
Db 505 GATTCAGCAATGGAAGAAGCAAACTTCTTCAAAATATGGATCTAAAGGTATTAATC 564
Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 565 CATAGAGAGATGCTTTTAGAGCGTCTAGATTATCGACAGCGAGCTTTGTCTAATCCT 624
Qy 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyTrpGlyAlaAsnGlyGly 226
Db 625 AAGATTGATGTGATTTGGAAGTCTGCTGTTGTGGAAGCTTATGGAGATGGAGAAAGAT 684
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 685 GTGCTTGGAGGATGAGAGTGAAGATGTGTTACCGAGAGATTTTCTGATTTAAAGTT 744
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 745 TCTGGATTGTTCTTGTCTATTGTCATGAGCCAGCTACCAAGTTTGTGGATGGTGTGTT 804
Qy 267 GluLeuAspSerAspGlyTyValGluThrLysProGlySerThrHisThrSerValLys 286
Db 805 GAGTTAGATTCCGATGGTATGTGTTGACGAAGCCCTGGTACTACAGACTAGCGTTCC 364
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyArgGlnAlaIleThrAlaAla 306
Db 865 CGAGTTTTCGCTCGCGGTGATGTTCAAGATAAGAGTATAGGCAAGCCATCACTGCTCA 924
Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyIleuGlnIleGlyAlaGln 326
Db 925 GGAATCGGGTGCATGCGAGCTTTGGATGTCAGAGCATTTACTTACAGAGATTGGATCTCAG 984
Qy 327 GluGlyLysSerAsp 331
Db 985 CAAGGTAAAGTGAAT 999
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RESULT 14

US-10-032-201B-10

; Sequence 10, Application US/10032201B

; Publication No. US20030167524A1

; GENERAL INFORMATION:

; APPLICANT: Van Rooijen, Gijb

```
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1002)
; OTHER INFORMATION: cDNA encoding NADPH thioresdoxin reductase
US-10-032-201B-10
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Alignment Scores:
Pred. No.: 5,01e-160 Length: 1002
Score: 1318.00 Matches: 254
Percent Similarity: 85.77% Conservative: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 1
DB: 15 Gaps: 1
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US-10-005-429-25 (1-331) x US-10-032-201B-10 (1-1002)

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Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyAlaAla 30
Db 25 ACAAGCTCTGTATAGAGTGGCCAGCGCCACACACGCGCGGCGATTACGCGAGCT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
Db 85 AGGGCTGAACCTTAACCTCTCTTCGAGAGGATGGATGCTAACGACATCGCTCCCGGT 144
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 145 GGTCACTAACACACCGAGCTGCGAGATTTCCCGGNTTCCAGAGGTATTC 204
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 205 CGAGTAGAGCTCACTGACCAATTCCTTAACATCGAGCGATTCGGTACTACGATATT 264
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysPropheArgValSerAlaAspSer 110
Db 265 ACHAGACGCTGACGAAGTCTGATTTCTTCGAACCGTTTAAGCTATTCACAGATTCA 324
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgLeuHis 130
Db 325 AAAGCCATTCTCGCTGACGCTGTGATTCGCTACTGAGCTGTGGCTGCGTAAAGCGGTAGC 384
Qy 131 Phe-----ProGlySerAspAlaTyTrpAsnArgGlyIleSerAlaCysAla 146
Db 385 TTCGTTGGATCTGGTGAAGTCTCGAGGTTTCTCGAACCGTGAATCTCCGCTTGTGCT 444
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 445 GTTTGCGAGGAGCTCTCCGATATTCGTTACCAAACTCTTCGCGTGTGATCGGTGAGGC 504
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyTrpAsnArgGlyIleLeu 186
Db 505 GATTCAGCAATGGAAGAAGCAAACTTCTTCAAAATATGGATCTAAAGGTATTAATC 564
Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 565 CATAGAGAGATGCTTTTAGAGCGTCTAGATTATCGACAGCGAGCTTTGTCTAATCCT 624
```

Sequence 37, Application US/09897425
 Publication No. US20020088025A1
 GENERAL INFORMATION:
 APPLICANT: MOLONEY, MAURICE M.
 APPLICANT: DALMIA, BIPIN K.
 TITLE OF INVENTION: PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
 TITLE OF INVENTION: PROTEINS ON OIL BODIES
 FILE REFERENCE: 034547/0106
 CURRENT APPLICATION NUMBER: US/09/897,425
 CURRENT FILING DATE: 2001-07-03
 PRIOR FILING DATE: 09/210,843
 PRIOR FILING DATE: 1998-12-18
 PRIOR APPLICATION NUMBER: 08/846,021
 PRIOR FILING DATE: 1997-04-25
 PRIOR APPLICATION NUMBER: 08/366,793
 PRIOR FILING DATE: 1994-12-30
 PRIOR APPLICATION NUMBER: 08/142,418
 PRIOR FILING DATE: 1993-11-16
 PRIOR APPLICATION NUMBER: 07/659,835
 PRIOR FILING DATE: 1991-02-22
 NUMBER OF SEQ ID NOS: 55
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 37

LENGTH: 1002
 TYPE: DNA
 ORGANISM: Arabidopsis sp.
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(999)
 US-09-897-425-37

Alignment Scores:
 Pred. No.: 5,01e-160 Length: 1002
 Score: 1318.00 Matches: 254
 Percent Similarity: 86.77% Conservative: 28
 Best Local Similarity: 78.15% Mismatches: 39
 Query Match: 77.12% Indels: 4
 DB: 13 Gaps: 1

US-10-005-429-25 (1-331) x US-09-897-425-37 (1-1002)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
 Db 25 ACAGGCTCTGTATCGTAGGAGTGGCCACGCGCACACACGCGGCGATTACGAGCT 84
 Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
 Db 85 AGGGCTGAACCTTAAACCTTCTCTTCGAAGGATGGATGCTTAACGACATCGCTCCCGT 144
 Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
 Db 145 GGTCAACTAAACACACACGCGAGCTCGAGAAATTTCCCGGATTTCGAGAGGATTCTC 204
 Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
 Db 205 GGAGTAGAGCTCACTGACAAATTCGTAAACAAATCGGAGCGATTCGGTACTACGATATT 264
 Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysPropheArgValSerAlaAspSer 110
 Db 265 ACAGAGCGGTGACGAAAGTGGATTCTTCGAAACCGGTTTAAGCTATTACAGATTCAC 324
 Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgLeuHis 130
 Db 325 AAAGCATTCGCTGACGCTGTGATTCTCGTACTGAGCTGTGGCTAAGCGGCTTAGC 384
 Qy 131 Phe-----ProGlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
 Db 385 TTCGTTGATCTGCTGAAGGTTCTGAGGTTCTGGAACCGTGAATCTCGCTGTGCT 444
 Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
 Db 445 GTTTCGAGGAGCTGCTCCGATATTCGTAAACAACTCTTGGCTGATCGGTGGAGGC 504

Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
 Db 505 GATTCAGCATGGAGAGCAAACTTCTTCAAAATATGGAATCTAAAGGTATATAATC 564
 Qy 187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaAlaArgAlaLeuGluAsnPro 206
 Db 565 CATAGCAGAGATCTTTTAGAGCGTCTAAGATTATGCAGCAGCGAGCTTTGTCTAATCCT 624
 Qy 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
 Db 625 AAGATTGATGTGATTGGAACTCTCTGTGTGGAAGCTTATGGAGATCGAGAAAGAGAT 684
 Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
 Db 685 GTCTTGGAGGATTGAAGTGAAGAATGTGTTACCGAGATGTTCTGATTTAAAGATT 744
 Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
 Db 745 TCTGGATTGTCTTCTTGTCTATGTCATGAGCCAGCTACCAAGTTTGGATGTGTGT 804
 Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
 Db 805 GAGTTAGATTGGATGTTATGTTGTCAGAGCGCTGGTACTACACAGACTAGCGTCCC 864
 Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
 Db 865 GGAGTTTTCGCTCGGGTGATGTTTCAGGATAAGAGTATAGGCAAGCCATCCTGCTGCA 924
 Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
 Db 925 GGAATCGGTGGTCATGGCAGCTTTGGATGAGAGCATTTACTTACAGAGATTGGATCTCAG 984
 Qy 327 GluGlyLysSerAsp 331
 Db 985 CAAGGTAAGAGTGTAT 999

RESULT 13

US-10-032-201B-8

Sequence 8, Application US/10032201B
 Publication No. US20030167524A1
 GENERAL INFORMATION:
 APPLICANT: Van Rooijen, Gijls
 APPLICANT: Deckers, Harm
 APPLICANT: Heifetz, Peter Bernard
 APPLICANT: Briggs, Steven
 APPLICANT: Dalmia, Bipin Kumar
 APPLICANT: Del Val, Greg
 APPLICANT: Zaplachinski, Steve
 APPLICANT: Moloney, Maurice
 TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
 TITLE OF INVENTION: COMPOSITIONS
 FILE REFERENCE: 38814 351B
 CURRENT APPLICATION NUMBER: US/10/032,201B
 CURRENT FILING DATE: 2001-12-19
 NUMBER OF SEQ ID NOS: 313
 SOFTWARE: Fast-Seq for Windows Version 4.0
 SEQ ID NO 8
 LENGTH: 1002
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-10-032-201B-8

Alignment Scores:
 Pred. No.: 5,01e-160 Length: 1002
 Score: 1318.00 Matches: 254
 Percent Similarity: 86.77% Conservative: 28
 Best Local Similarity: 78.15% Mismatches: 39
 Query Match: 77.12% Indels: 4
 DB: 15 Gaps: 1

US-10-005-429-25 (1-331) x US-10-032-201B-8 (1-1002)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30

Db 565 CATAGGAGATGCTTTAGAGCTCTAAGATTATGACAGCGAGCTTTGCTAATCCT 624
Qy 207 LysileLeuValLeuThrAspSerGluValValGluAlaThrGlyGlyAlaAsnGlyGly 226
Db 625 AAGATTGATGCTGATTTGGAACTGCTGTTGTTGGAAGCTTATGGAGATGGAGAAGAGAT 684
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuAlaAsnGlyGlyValSerAspLeuGlnVal 246
Db 685 GTGCTTGGAGGATTGAAGTGAAGATGTTGTTACCGGAGATGTTCTGATTTAAAGTT 744
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
Db 745 TCTGGATTCTCTTCTGCTATGCTATGCTATGACGAGCTACCAAGTTTGTGATGCTGCTGT 804
Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 805 GAGTTAGATTCGATGCTGTTGTTGTCAGAGAGCTTGGTACTACAGACTAGCTTCC 864
Qy 287 GlyValPheAlaGlyAspValGlnAspLysLysLysLysLysLysLysLysLysLys 306
Db 865 GGAGTTTTCGCTCGCGGCTGATGTTTCAGGATAAAGATATAGGCAAGCCATCACTGCTGCA 924
Qy 307 GlySerGlyCysMetAlaAlaLeuAlaLeuAlaGluHisLysLysLysLysLysLys 326
Db 925 GGAATCGGCTGATGCTGCTTGGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 984
Qy 327 GluGlyLysSerAsp 331
Db 985 CAAGGTAAGATGAT 999

RESULT 11

US-09-897-425-36
; Sequence 36, Application US/09897425
; Publication No. US2002068025A1
; GENERAL INFORMATION:
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMA, BIPIN K.
; TITLE OF INVENTION: PREPARATION OF THIOREDIXIN AND THIOREDIXIN REDUCTASE
; TITLE OF INVENTION: PROTEINS ON OIL BODIES
; FILE REFERENCE: 034547/0106
; CURRENT APPLICATION NUMBER: US/09/897,425
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/210,843
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/846,021
; PRIOR FILING DATE: 1997-04-25
; PRIOR APPLICATION NUMBER: 08/366,783
; PRIOR FILING DATE: 1994-12-30
; PRIOR APPLICATION NUMBER: 08/142,418
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 07/859,835
; PRIOR FILING DATE: 1991-02-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Published NADPH
; OTHER INFORMATION: thioredoxin reductase sequence
; NAME/KEY: CDS
; LOCATION: (1)..(999)
US-09-897-425-36

Alignment Scores:

Pred. No.:	5,01e-160	Length:	1002
Score:	1318.00	Matches:	254
Percent Similarity:	86.77%	Conservative:	28
Best Local Similarity:	78.15%	Mismatches:	39
Query Match:	77.12%	Indels:	4
DB:	13	Gaps:	1

RESULT 12

US-09-897-425-37

US-10-005-429-25 (1-331) x US-09-897-425-36 (1-1002)
Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleThrAlaAla 30
Db 25 ACAAGGCTCTGATGCTAGGAGTGGCCAGCGGCACACAGCGCGCGGATTTTACCAGCT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
Db 85 AGGCTGAACCTTAAACCTCTCTCTCGAAGATGATGGCTAACGACATGCTCCCGT 144
Qy 51 GlyGlnLeuThrThrThrThrAspValGlnAsnPheProGlyPheProAsnGlyIleMet 70
Db 145 GGTCAACTAACACACACCGAGCTCGAGAATTTCCCGGATTTCCAGAAAGTATTCTC 204
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 205 GGATGAGCTCAGTACAAATTCGTAAACATCGGAGCGATTCGGTACTACGATATT 264
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 265 ACAGAGCGGTGACGAAAGTTCGATTTCTCTTCGAAACCGTTTAAGCTATTACAGATTCA 324
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArgLeuHis 130
Db 325 AAAGCCATCTCCCTGACGCTGTGATTTCTGCTACTGAGCTGTGCTGAGCGGTAGC 384
Qy 131 Phe-----ProGlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 385 TTCGTTGGATCTGCTGGAAGTTCTCGAGGTTCTCGAACCGTGAATCTCCGCTGTGCT 444
Qy 147 ValCysAspGlyAlaAlaPheArgLeuPheProIleAlaValIleGlyGlyGly 166
Db 445 GTTTCGACGAGCTGCTCCGATATTCGTAAACACCTCTTCGCGGTATCGGTGAGGC 504
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValIleIle 186
Db 505 GATTCAGCAATGGAAGAAGCAACCTTCTTCAAAATATGGATCTAAAGTGTATATAATC 564
Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 565 CATAGGAGATGCTTTTAGAGCGTCTAAGATTATGACGACGCGAGCTTTGCTAATCTCT 624
Qy 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyAlaAsnGlyGly 226
Db 625 AAGATTGATGCTGTTGGAACTGCTCTGTTGGAGCTTATGGAGATGGAGAAGAGAT 684
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 685 GTGCTTGGAGGATTCGAAAGTGAAGATGCTGTTACCGGAGATGTTTCTGATTTAAAGTT 744
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
Db 745 TCTGATTTGTTCTTTGCTATTGCTCATGAGCGAGCTACCAAGTTTGTGATGCTGCTGT 804
Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 805 GAGTTAGATTCGATGCTTATGTTGTTGTCAGAGCTGCTTACTACAGACTAGCTTCC 864
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysLysLysLysLysLysLysLysLys 306
Db 865 GGAGTTTTCGCTCGCGGCTGATGTTTCAGGATAAAGATATAGGCAAGCCATCACTGCTGCA 924
Qy 307 GlySerGlyCysMetAlaAlaLeuAlaLeuAlaGluHisLysLysLysLysLysLys 326
Db 925 GGAATCGGCTGATGCTGCTTGGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 984
Qy 327 GluGlyLysSerAsp 331
Db 985 CAAGGTAAGATGAT 999


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; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_30236C.1
US-10-424-599-65583

Alignment Scores:
Pred. No.: 9,1e-160 Length: 1645
Score: 1318.50 Matches: 253
Percent Similarity: 88.38% Conservatives: 36
Best Local Similarity: 77.37% Mismatches: 33
Query Match: 77.15% Indels: 5
DB: 13 Gaps: 2

US-10-005-429-25 (1-331) x US-10-424-599-65583 (1-1645)
QY 10 ArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAla 29
DB 166 AGACCAAACTCTGCATCATCGAAGCGGTCTCTCCGCCACACACAGCGCGGTACGGCC 225
QY 30 AlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAla 49
DB 226 GCTCGAGCGGAGCTGAAGCGCATCTCTTCGAGGGCTGGATGSCCAACGACATCGCCGCC 285
QY 50 GlyGlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIle 69
DB 286 GCGCGCCAGCTACACACACACCGACGTCGAGAACTTCCCGGGTTCGCCGAGGCATC 345
QY 70 MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle 89
DB 346 CTCGCGCGGAGCTCATAGGAAGCTCCCGAGGACGTCGCTCGCTTCGGCACCGAGATC 405
QY 90 LeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp 109
DB 406 CACCCGAGACGCTCTCCAAAGTTCGATTTCTCGAACCGTCTTTCAGGGTTTTCACCGAT 465
QY 110 SerThrThrValLeuAlaAlaValIleValAlaThrGlyValAlaAlaArgArgLeu 129
DB 466 TCCGACCAAGCTCGAGCGCAATCCGTCATCGTCGCCACCGCGCGCTCGCCAAAGCGCCTC 525
QY 130 HisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCys 145
DB 526 CCGCTTCCCGGCTCCGCGAGTGGCCCGGAGTGGTCTCGAACCGCGGATCTCCCGGTGC 585
QY 146 AlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 165
DB 586 GCGCTCTGCGATGCGCGCGCGGATCTTCGGAACCAAGCCATCGCGGTGATCGCGCGC 645
QY 166 GlyAspSerAlaMetGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIle 185
DB 646 GGGGACTCGCGATGAGGAGCGCCACTTCTCCTCACCAGTACGGTTCCGAGGTTTACATA 705
QY 186 IleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsn 205
DB 706 ATTCCCGAGGATACATTCAGGGCTTCGAAGATTATCGAGCAAGGTTATGGGCAAT 765
QY 206 ProLysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyAla---Asn 224
DB 766 AGCAGATTAAAGTGATTTGGAATTCCGTGGTGGTTGAGGCTTTTGGGGCGGAGATAAC 825
QY 225 GlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeu 244
DB 826 AGAGGGTGCTTGGGGATGAGGTTAGAGGTTAGAAAGTGGTCTCGAGAGGTATCTGAATG 885
QY 245 GlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGly 264
DB 886 AAGTTCTTGGGTGTGTTTTCGCAATTGGCAGCGAGCCCGCAGTTCCTTGGACGGG 945
QY 265 GlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSer 284
DB 946 CAGCTTGAATTGATTTCTGATGATATATTTGACGAAGCCCGGGAGCAGCAAGACAGT 1005
QY 285 ValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThr 304
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DB 1006 GTTAGGGAGGTTTGTCTGCTGGGGATGTTTCAGGACAGAGATATAGGCAAGCTATTACT 1065
QY 305 AlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGly 324
DB 1066 GCTGCTGGCACTGGATGCATGGCTGCTTTGGATGCAGAACATTACTCTGCAAAATGTTGTT 1125
QY 325 AlaGlnGluGlyLysSerAsp 331
DB 1136 TTACAACAAGATAAGATGAT 1146
RESULT 9
US-09-897-898-1
; Sequence 1, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GIJS
; APPLICANT: BOOTHE, JOSEPH
; APPLICANT: GOLL, JANIS
; APPLICANT: MCLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: THIOREDOLIN AND THIOREDOLIN REDUCTASE CONTAINING OIL
; TITLE OF INVENTION: BODY BASED PRODUCTS
; FILE REFERENCE: 034547/0104
; CURRENT APPLICATION NUMBER: US/09/897,898
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/577,147
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/448,600
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/084,777
; PRIOR FILING DATE: 1998-05-27
; PRIOR APPLICATION NUMBER: 60/047,753
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: 60/047,779
; PRIOR FILING DATE: 1997-05-28
; PRIOR APPLICATION NUMBER: 60/075,863
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/075,864
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patents in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(999)
; OTHER INFORMATION: Description of Unknown Organism: Published NADPH
; OTHER INFORMATION: thioredoxin reductase
US-09-897-898-1
Alignment Scores:
Pred. No.: 5,01e-160 Length: 1002
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservatives: 28
Best Local Similarity: 78.13% Mismatches: 39
Query Match: 77.12% Indels: 4
DB: 9 Gaps: 1
US-10-005-429-25 (1-331) x US-09-897-898-1 (1-1002)
QY 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 25 ACAAGGCTCTGATGTAGGAAGTGGCCCGGACACACACCGCGGATTTACGAGCT 84
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
DB 85 AGGGCTGAACCTTAAACCTCTCTCTCGAGGATGATGCTTAACGACATCGTCCCGGT 144
QY 51 GlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
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QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
Db ATGGAGGGATCCCGCGGGCGCGCTCCGACGCGCTGTGATCATCGGAGCGGGCG 465
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db TCGGCGCACACGCGCGGAGTCTACGCGCGCGCGCGGAGCTCAAGCGCGCTGTCTCTCGAG 525
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrThrThrThr 60
Db GGCTGCTCGCCACACGACATCGCGCGCGGGGGGCGAGCTCACACACACACGCGCGTCCGAG 585
QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
Db AACCTCCCGGGGTTCGCCGAGGGATCTTCGCGCGGAGCTCATGATCGTGGCGCGCG 645
QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
Db CAGTCCCTCCGGTTCGGCCAGCATCTCTCGAGACCGTCAACCGCGTCACTCTCC 705
QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db GCCCGCCCTTCGCGGTCCGCTCCGACTCCACACCGTCTCGCGAGCGCGTGGTGGTC 765
QY 121 AlaThrGlyAlaValAlaArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
Db GCCACCGGCGCGTCCCGCGGACTCCACTTCGCGGCTCCGACGCTTACTGGAACCGC 825
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db GGCATCTCAGCTGCGCGCTCTCGAGCGGGCGCGCCCAATCTTCAGGAACAACCCATC 885
QY 161 AlaValIleGlyGlyGlyAspSerAlaMetGluSerAsnPheLeuThrLysTyrGly 180
Db GCCGTTCATCGCGCGCGGACTCCGCGCATCGGAGGAGTCCAACTTCCTCAACGTAACGCG 945
QY 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db TCCATGTGTATCATATCATCCGCCGCCACACCTTCGCGGCTCCCAAGATCATCGAGCGC 1005
QY 201 ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyr 220
Db AGGGCGTTGTCAAAACCCCAAGATCCAGGTTTCTCGGAGCTCTGAGGTCTCGAGGCGCTAC 1065
QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysValLysLeuAsnGlyGlu 240
Db GCGCGCGAGGGTGGAGTCCATTTGGCTGGTGTCAAGTGAAGACTTGGTACTCGGGAAG 1125
QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db ATCTCCGACCTTCAGGTGTCCGCTCTCTCTCTTCGCCATCGGACATCAACCGCGGACGAAG 1185
QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
Db TTCTCGCGGGGAGCTTGAAGGGGCTCTTGTGCTGGTATGTGGCCACCAAGCGAGCTCC 1245
QY 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
Db ACGCACACAGTGTGAAGGGGCTCTTGTGCTGGGGA1GTGCAGACGAAGATATCCG 1305
QY 301 GlnAlaIleThrAlaAlaGlySerGly 309
Db CAGGCTATTACTGCGCGCTGATCAGGT 1332

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RESULT 6

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US-09-938-842A-2486
; Sequence 2486, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong

```

```

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2486
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-2486

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Alignment Scores:

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Pred. No.: 3,38e-162 Length: 1152
Score: 1335.50 Matches: 258
Percent Similarity: 86.65% Conservative: 34
Best Local Similarity: 76.56% Mismatches: 36
Query Match: 78.15% Indels: 9
DB: 9 Gaps: 2

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US-10-005-429-25 (1-331) x US-09-938-842A-2486 (1-1152)

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QY 4 SerAlaAlaAlaProLeu-----ArgThrArgIleCysIleIleGlySer 18
Db TCCGCGCGCGCGCGCTCGACATGGAAACTCACAACCAAGGTTTGCATCGCGAAGT 198
QY 19 GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38
Db GGACGAGGAGCACACACGCGCGGAGTCTATGATCATCGAGCGGAGCTTAAGGCTCTTCTC 258
QY 39 PheGluGlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrThr 58
Db TTCGAGGATGGATGGCTTAACGACATCGCTCCCGCGGCTCAATTAACTACACAACCGAC 318
QY 59 ValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCys 78
Db GTCCGAAATCTTCCCTGGGGTCCCTGAAGTATATTCGCGATTTGATGATCGTGAGAAATTC 378
QY 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAsp 98
Db AGAAACATCGGAGAGATTTGGAACATCGATCTTCACGGAACCTGTTAACAAAGTTGAT 438
QY 99 PheSerAlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
Db TTCTCATCGAAACCGCTTTAAGCTATTCACTGATTCGAGAACTGTTCGCTGATTTCTGTA 498
QY 119 IleValAlaThrGlyAlaValAlaAlaArgLeuHisPheProGlySer----- 134
Db ATCATTTCTACTGGAGCTGTGCTAAAGCTCTTAGCTTCACTGGATCTCGTGAAGGTAAT 558
QY 135 AspAlaTyrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
Db GGTGGTGTTCGAACTCGGTGATCTCCGCTTGCTGTGCTTTGCGACGAGCTCTCCGAT 618
QY 155 PheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMetClnGluSerAsn 174
Db TTTAGGAATAAGCTCTTGTGGTATTATGGTGTGATTCAGCTATGAGGAGGAGGAAAT 678
QY 175 PheLeuThrLysTyrGlySerHisValTyrIleIleHisArgAsnThrPheArgAla 194
Db TTTCTGACTAAGTATGGATTAAGGTTTATATTATCATAGGAGGATACGTTTAGGGCG 738
QY 195 SerLysIleMetGlnAlaArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSer 214
Db TCTAAGATTATCGACGAGAGCTTTGTCTAACCCCTTAAGATTGAAGTATTGGAACTCT 798
QY 215 GluValValGluAlaTyrGlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLys 234

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; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2486
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-2486

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Db      959 GCAGGAGTGGGTGCACACAGGTGGGCAAGTCTGAT 992
US-10-091-841-23
; Sequence 23, Application US/10091841
; Publication No. US20030150010A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; TITLE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/10/091,841
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-091-841-23

Alignment Scores:
Pred. No.: 7,49e-185 Length: 995
Score: 1510.00 Matches: 302
Percent Similarity: 93.98% Conservative: 10
Best Local Similarity: 90.96% Mismatches: 19
Query Match: 82.36% Indels: 3
DB: 15 Gaps: 0

US-10-005-429-25 (1-331) x US-10-091-841-23 (1-995)

Qy      1 MetGluGlySerAlaValCysAspGlyValAlaProIlePheArgAsnLysProIle 20
Db      1 ATGGAGGGATCGCGCGCGCGCGCGCTCCGACGCGGTGTCATCATCGCGCGCGCG 60
Qy      21 AlaAlaHisThrAlaAlaIleThrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db      61 GCCGGGACACGCGCGCGCATCTACGCGCGCGCGCGCGGAGCTCAAGCGGTGCTCTTCGAG 120
Qy      41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrThrThrThr 60
Db      121 GCTTGGATGGCCACGACATCGCGCGGGGSCCAGCTCACCACACACCGACGTCGAG 180
Qy      61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
Db      181 AACTTCCCGGATTCGCCACCGGCATCATGGGCATCGACCTCATGACAACTGCGCGGCC 240
Qy      81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
Db      241 CAGTCCGTCGCGGTGGACACCAACATCTCTCCGAGACGTCACCGAGGTGCACTTCTCC 300
Qy      101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db      301 GCCCGGCCCTTCGGGTCACTCCCGACCTCCGACCGCTCTCGCGACACCGTCTGCTGTC 360
Qy      121 AlaThrGlyAlaValAlaArgGluHisPheProGlySerAspAlaIleThrIleAsnArg 140
Db      361 GCCACGGCGCGCGTCCGCGCGCGCGCTCCATTTCTCGGTTTCCGACACTTCTGGACCGC 420

141 GlyIleSerAlaCysAlaValCysAspGlyValAlaProIlePheArgAsnLysProIle 160
161 AlaValIleGlyGlyGlyAspSerAlaMetGluSerAsnPheLeuThrIleLysThrGly 180
481 GCCTTCATCGCGCGCGGTGATTCCGCGCATGGAGGAAGGCAACTTCTCTCACCAAGTACGGA 540
181 SerHisValTyrIleIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
541 TCCCAAGTGTACATCATCCACGCGCGCGCACACCTTCCGCGCTCCCAAGATTATGAGGCT 600
201 ArgAlaLeuGluAsnProLysIleLysValLeuThrAspSerGluValValGluAlaTyr 220
601 AGGCGGCTCTCCCAATCTCAAGATCCAGGTTGTCTGGGACTC-GAGGTGCTCGAGGGCTTAC 659
221 GlyValAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
660 GCGGTGACGCGCGCGCGCATTTAGTGGGTCAAGTCAAGAACTTGGTCACTGGTGAG 719
241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
720 GTGTCTGACCTTCAGGTGTCCGGCTTTTCTTCCGACATCGGCGCATGAGCGCGGCCCAAG 779
261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
780 TTTCTCAATGGCAGCTTGAGCTCCATGCGGATGGGTATGTGCCCAACAGCCGCGCTCT 839
281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
840 ACACATACCAAGTGTGGA-GGGGTCTTTGCTGTGGACAGCTGCAGGATAAGAAGTATCGT 898
301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrLe 320
899 CAGGCCATTACTGCTGTGATCATAGTTGATGCTCTTGGACCGCGGACGACTATCT 958

320 uGlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
959 GCAGGAGTGGGTGCACAGGTGGGCAAGTCTGAT 992

RESULT 5
; Sequence 26, Application US/10306292
; Publication No. US20030145347A1
; GENERAL INFORMATION:
; APPLICANT: Lahanan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gadsdask, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/10/306,292
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/598,747
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-306-292-26

Alignment Scores:
Pred. No.: 2.02e-180 Length: 1560
Score: 1478.00 Matches: 282
Percent Similarity: 96.12% Conservative: 15
Best Local Similarity: 91.26% Mismatches: 12
Query Match: 86.48% Indels: 0
DB: 15 Gaps: 0

US-10-005-429-25 (1-331) x US-10-306-292-26 (1-1560)
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QY 161 AlaValIleGlyGlyVasppSerAlaMetGluGluSerAsnPhelThrLysTyrGly 180
DB 567 GCCGTCATAGCGCGCGGACCTCCGCTATGAGGAGTCCAAITTCCTCACCAGTAACGCGC 626
QY 181 SerHisValTyrIleIleHisArgArgenThrPheArgAlaSerIleIleMetGlnAla 200
DB 627 TCCACAGCTACATCATCCACCGCGCAATACCTCCGTCCTTCCAGATCATGAGGCC 686
QY 201 ArgAlaLeuGluAsnProLysIleLysValLeuTTPAspSerGluValValGluAlaTyr 220
DB 687 AGGGGCGCTTGAGAACCCCAAAATTAAGGTCTCTCGGACTCGGAAGTTGTGAGGCTTAT 746
QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuAsnGlyGlu 240
DB 747 GCGCGCGCAAAACGCGCGCCCATTTGCTGCGGTAAAGGTTAAGAACCTACTGAATGGTGAG 806
QY 241 ValSerAspLeuGluValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
DB 807 GTCTCGAGTCCTCAGGTGTCTGCTCTCTCTTCGCGCATCGGCGATGAGCGCGGACCAAA 866
QY 261 PheLeuGlyGlyGluLeuLeuLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
DB 867 TTCTCGGCGGACAGCTTGAATTCGATTCGATGGTGTATGTGGAACCAAGCCAGGTTCC 926
QY 281 ThrHisThrSerValLysGlyValPheAlaIleGlyValGluAspValGlnAspLysTyrArg 300
DB 927 ACTCACACAGGTAAAGGTTATTTGCTGCTGGGACGTGCGAGCAAGAGTACCGT 986
QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
DB 987 CAGGCCATTAATTCGCGTGCATCAGGGTGCATGGTGCATTCGACGCTGAGCACTACCTG 1046
QY 321 GlnGluIleGlyAlaGlnGluLysSerAsp 331
DB 1047 CAGGAGATCGGTGCACAGGAGGAAAGTCTGAT 1079

RESULT 3
US-10-091-841-10
; Sequence 10, Application US/10091841
; Publication No. US20030150010A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillau, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; FILE OF INVENTION: NADP-Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/10/091,841
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-091-841-10

Alignment Scores: 7.49e-185 Length: 995
Pred. No.: 1510.00 Matches: 302
Score:
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Percent Similarity: 93.98% Conservative: 10
Best Local Similarity: 90.96% Mismatches: 19
Query Match: 88.36% Indels: 3
DB: 15 Gaps: 0

US-10-005-429-25 (1-331) x US-10-091-841-10 (1-995)

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DB 1 ATGAGGGATCCCGCGCGCGCCCTCCGACCGCGGTGTGCATCATCGGAGCGGCCG 60
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
DB 61 GCGCGGCACACGCGGCGCATCTACGCGCGCGCGGAGCTCAAGCGGTCTCTCTCGAG 120
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrThrThrThr 60
DB 121 GCGTGGATGGCAACGACATCGCGCGCGGCGGCGGCTCACCCACCAACGCGCTCGAG 180
QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
DB 181 AACTTCCCGGATTTCCCGCGGATCATGCGGCTCATGACCTCATGGACAACATGCGCGC 240
QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
DB 241 CAGTCCGTCGCTTCGCGCACCAACATCTCTCCGAGACCGTCACCGAGGTGACTTCTCC 300
QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
DB 301 GCGCGCCCTTCGCGGTCCCTCCGACCTCCACCGCTCTCCGCGACCGCTCGCTCGCTC 360
QY 121 AlaThrGlyAlaValAlaArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
DB 361 GCCACGCGCGCGTCCGCGCGCTCCATTTCTCCGTTCCGACACCTACTTGGAAACCGC 420
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
DB 421 GGCATCTCCGCTGCGCGCTGCGACGCGCTGCGCCCATCTTCCGGAACAAGCCCATC 480
QY 161 AlaValIleGlyGlyVasppSerAlaMetGluGluSerAsnPheLeuThrLysTyrGly 180
DB 481 GCGTTCATCGCGCGCGGTGATTCCGCGATGAGGAGGCAACTTCTCTCACCAGTAACGGA 540
QY 181 SerHisValTyrIleIleHisArgArgenThrPheArgAlaSerLysIleMetGlnAla 200
DB 541 TCCCAAGTGTATCATCATCCACGCGCGCAACCTTCCGCGCTCCAGATTTATGAGGCT 600
QY 201 ArgAlaLeuGluAsnProLysIleLysValLeuTTPAspSerGluValValGluAlaTyr 220
DB 601 AGGCGCTCTCATCTCCATCCAGTCCAGGTCTCTGGGACTC-GAGTCTCTGAGGCTTAC 659
QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuAsnGlyGlu 240
DB 659 GCGGTGCGAGCGCGCGCCCATTAGCTGGGTCAAGGTCAAGACTTGGTGTGCTGTGAG 719
QY 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
DB 720 GTGCTGACCTTCAGGTGTCGCGGTCTTCTTCGCGCATCGGCGCATGAGCGGCCACCAAG 779
QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
DB 780 TTTCTCAATGGGACGCTTGAAGTCCATGCGGTATGTGGTCCACCAAGCGGCTCT 839
QY 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysTyrArg 300
DB 840 ACACATACAGTGTGGA-GGGGTCTTTGCTGCTGAGACGTGAGGATAAGAGTATCGT 898
QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaGluHisTyrLe 320
DB 899 CAGGCCATTAATTCGCTGCTGATCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 958
QY 320 uGlnGluIleGlyAlaGlnGluLysSerAsp 331
DB 958
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US-10-425-114-5073

Alignment Scores:

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Score: 1709.00 Matches: 331
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-005-429-25 (1-331) x US-10-425-114-5073 (1-1286)

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Db 58 ATGGAGGATCGCGCGCTCGCTCGCGAGCGCATCTGCATCATCGGAGCGGTCCC 117
Qy 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db 118 GCTGGCAGACGGGAGCGCATCTAGCGCGCGCGCGGAGCTCAAGSCCTGTGCTCTTCGAG 177
Qy 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrAspValGlu 60
Db 178 GCTGGATGGCCACGACATCGCGCGCGCGGCGGAGCTCACCACCAACCGAGGTGCGAG 237
Qy 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
Db 238 AACTTCCCGGCTTCCCAACGGCATCATGGCGCGCGGACCTCATGGCACTGCGCGCGG 297
Qy 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
Db 298 CAGTCCCTGCGCTTGGCAGCAACATCTCTCCGAGACCGTCCACCGCTGCATTTTCG 357
Qy 101 AlaCysProPheArgValSerAlaAspSerThrValLeuAlaAspAlaValIleVal 120
Db 358 GCCTGCCCATTCGAGTGTAGTGCAGACTCCCAACCGCTCTCGCGGATGCGGTATCGTT 417
Qy 121 AlaThrGlyAlaValAlaArgArgGluHisPheProGlySerAspAlaTyrTrpAsnArg 140
Db 418 GCCACGGAGCGGTGCGCGCGCTCCATCTCCCGGGTCCGATGATCATCTGGAACCGC 477
Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 478 GGCACTCTCGCTGTGCGCTCTGTGAGCGTGGCGCGCCCATCTTCGTAACAAGCCCATC 537
Qy 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrIleTyrGly 180
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Qy 201 ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyr 220
Db 658 AGGCGCTTGAGAACCCCAAAATTAAAGTCTCTGGGACTCGGAAGTTGTTCGAGCCCTAT 717
Qy 221 GlyGlyAlaAsnGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
Db 718 GCGCGCGCAACCGCGGCCCATTTGGCTGGCTGAAGGTTAAGACCTACTGATGATGGTGG 777
Qy 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
Db 778 GTCTCGGATCTTCAGGTCTGGCTCTCTTCGCGCATCGGCGCATGAGCGCGCGCAAAA 837
Qy 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
Db 838 TTCTTGGCGGACACCTTGAACTCGATTCAGATGGTTATGTTGGAACCAACCCAGGTTC 897
Qy 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
Db 898 ACTCACACAGGTAAAGGGTGTATTGTCTGCTGCGGACGTCGACGACAAAGAGTACCGT 957
Qy 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320

Db 958 CAGCCATTACTGCGCTGGATCAGAGGTGCATGGCTGCATTCGATTCGAGCACTACCTG 1017
Qy 321 GlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
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RESULT 2
US-10-425-114-3716
; Sequence 3716, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven B.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3716
; LENGTH: 1325
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700336177_FLI
US-10-425-114-3716

Alignment Scores:

Pred. No.: 2,17e-210 Length: 1325
Score: 1709.00 Matches: 331
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-005-429-25 (1-331) x US-10-425-114-3716 (1-1325)

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Db 87 ATGGAGGATCGCGCGCTCGCTCGCGAGCGCATCTGCATCATCGGAGCGGTCCC 146
Qy 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db 147 GCTGCGCACACGGCAGCCATCTAGCGCGCGCGCGGAGCTCAAGCCTGTGCTCTTCGAG 206
Qy 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
Db 207 GGCTGGATGGCCACGACATCGCGCGCGGCGGAGCTCACCACCAACCGAGCTCGAG 266
Qy 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
Db 267 AACTTCCCGGCTTCCCAACGGCATCATGGCGCGCGGACCTCATGGCACTGCGCGCGG 326
Qy 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
Db 327 CAGTCCCTGCGCTTGGCAGCAACATCTCTCCGAGACCGTCCACCGCTGCAGCTTTTCG 386
Qy 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db 387 GCCTGCCCATTCGAGTTAGTGCAGACTCCCAACCGTCTCCGCGATGCGGTATCGTT 446
Qy 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
Db 447 GCCACGGAGCGGTGCGCGCGCTCCATCTCCCGGGTCCGATGATGATCATGGAACCGC 506
Qy 141 GlyIleSerAlaCysAlaValCysAspGlyValAlaAlaProIlePheArgAsnLysProIle 160
Db 507 GGCACTCTCCGCTGTGCGCTGTGAGCGGTGCGCGCCCATCTTCGTAACAAGCCCATC 566

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 04:58:09 ; Search time 452.681 Seconds
(without alignments)

3307.557 Million cell updates/sec

Title: US-10-005-429-25

Perfect score: 1709

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -QWFI=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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RESULT 1

US-10-425-114-5073

Sequence 5073, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Jiongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

PLANT INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 5073

LENGTH: 1286

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: 700447274_FLI

ALIGNMENTS

1	1709	100.0	1286	13	US-10-425-114-5073	Sequence 5073, Ap
2	1709	100.0	1325	13	US-10-425-114-3716	Sequence 3716, Ap
3	1510	88.4	995	15	US-10-091-841-10	Sequence 20, Appl
4	1510	88.4	995	15	US-10-091-841-23	Sequence 23, Appl
5	1478	86.5	1560	15	US-10-306-292-26	Sequence 26, Appl
6	1335.5	78.1	1152	9	US-09-938-842A-2486	Sequence 2486, Ap
7	1335.5	78.1	1152	11	US-09-938-842A-2486	Sequence 2486, Ap
8	1318.5	77.2	1645	13	US-10-424-599-65583	Sequence 65583, A
9	1318	77.1	1002	9	US-09-897-898-1	Sequence 1, Appl
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11	1318	77.1	1002	13	US-09-897-898-36	Sequence 36, Appl
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13	1318	77.1	1002	15	US-10-032-201B-8	Sequence 8, Appl
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19	1318	77.1	4545	9	US-09-897-898-18	Sequence 18, Appl
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22	1318	77.1	4546	9	US-09-897-898-15	Sequence 15, Appl
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25	1318	77.1	6357	13	US-10-290-072-38	Sequence 38, Appl
26	1318	77.1	6357	13	US-10-290-072-42	Sequence 42, Appl
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28	1318	77.1	6357	15	US-10-141-531-42	Sequence 42, Appl
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30	1306	76.4	6357	13	US-10-290-072-35	Sequence 35, Appl
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32	1306	76.4	6357	15	US-10-141-531-35	Sequence 35, Appl
33	1306	76.4	6357	15	US-10-141-531-45	Sequence 45, Appl
34	1305	76.4	6357	13	US-10-290-072-37	Sequence 37, Appl
35	1305	76.4	6357	15	US-10-141-531-37	Sequence 37, Appl
36	1304	76.3	1345	13	US-10-290-072-215	Sequence 215, App
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39	1304	78.3	6357	13	US-10-290-072-44	Sequence 44, Appl
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42	1304	76.3	6357	15	US-10-141-531-44	Sequence 44, Appl
43	1303	76.2	6357	13	US-10-290-072-43	Sequence 43, Appl
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45	1303	76.2	6357	15	US-10-141-531-43	Sequence 43, Appl

Qy	284	SerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIle	303
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Qy	304	ThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrIeuGlnGluIle	323
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Search completed: May 5, 2004, 09:02:42
Job time : 4713.61 secs

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598 ATC---ATTCTGCACCAACCGTACGCTGGAAGAGTGAAGTGAAGTGAAGTGAAGTGA 651
228 LeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu---ValSerAspLeuGlnVal 246
652 GTCACTGCGGTGCTGCTGCGGATACGCAAAACGCGATACATCGATCGATCGATCG 711
247 SerGlyPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
712 GCGGCTGCTGTTGTGCTATCGCTCACAGCCCAATCTGCGATTTTCGAAAGGCGAGCTG 771
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283 ThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAla 302
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RESULT 15

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US-03-328-352-3988
; Sequence 3988, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04

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; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3988
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3988

Alignment Scores:
Pred. No.: 6,48e-75 Length: 954
Score: 703.50 Matches: 144
Percent Similarity: 64.38% Conservative: 62
Best Local Similarity: 45.00% Mismatches: 97
Query Match: 41.16% Indels: 17
DB: 4 Gaps: 6

US-10-005-429-25 (1-331) x US-09-328-352-3988 (1-954)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 16 TCACGCTCTGATAATCTCGGTTCTGGCCCTTCGGGCTATAGTCGACGATATATGACG 75
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
Db 76 CGTCAACCTTAAACCTACTTTAATTCAGGT-----TTACAGCTTGGC 120
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 121 GGCAACTTCAACACACACGAGTTCACAACTGGCGCGGCGATCTCTGAAGTTTAAACA 180
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 181 GGTCTGCTAATGAGTTCGTATGCAAGCACATGCTGAAGCTTTGGTACAGAACTCGTC 240
Qy 91 SerGlyThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 241 TATGACCATATTAACGAGTGGACTTAATATGCTAGCTCTTCGTTCTTAAAGGTGATATG 300
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArgLeuHis 130
Db 301 GAAGAGTACATGATGCTGCTTATGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Qy 131 PheProGlySerAspAlaTyrTyrAsnArgGlyIleSerAlaCysAlaValCysAspGly 150
Db 361 CTACAGTCTGAACAAACCTTTATGGGCAAGCGTAAAGCGCATGTGCAACATGTGATGGT 420
Qy 151 AlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGlyAspSerAlaMet 170
Db 421 TTC-----TTCACAAACCAACAAAGTAAATGCTGCTGCTGCTGCTGCTGCTGCTG 474
Qy 171 GluGlnSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIleHisArgArgAsn 190
Db 475 GAAGAGCAGCTTTATTTATCAATATTCCTTCACATGTAACGCTAGTACACCGCGGTGAT 534
Qy 191 ThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeu-----GluAsnProLys 207
Db 535 AGCTTACGCTTGAAGAAAGATTTTCAAGATCATTTATTTGTCAAAGAAAAAGAGGAAA 594
Qy 208 IleLysValLeuThrAspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGlyPro 227
Db 595 ATCAGCATTCGTAATCAGAACTGCAAGAGTATGAGAGTATGAGTATGAGTATGAGTAT 648
Qy 228 LeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnValSer 247
Db 649 GTAACAGTGTTCGCTTAAATCAACCAAGATGAATCAAGCAAGACGCTAGAGGTTCAT 708
Qy 248 GlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnGlu 267
Db 709 GGTCTATTCGTTGCAATGCTGCAACCAACCAATCTGCTGCTGCTGCTGCTGCTGCTG 769
Qy 268 LeuAspSerAspGlyTyrValGluThrLysProGly-----SerThrHisThr 283
Db 769 TTA---CGTGTGCTATATCAAGTACAAAGCGGTACTTCTGCTAATGCAACGACCAACC 825

```


PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/AU98/01023
 FILING DATE: 10-DEC-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Monroy, Gladys H
 REGISTRATION NUMBER: 32,430
 REFERENCE/DOCKET NUMBER: 27340-20021.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-813-5600
 TELEFAX: 650-494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 685:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1443 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEetical: NO
 ANTI-SENSE: UNKNOWN
 ORIGINAL SOURCE:
 ORGANISM: PORPHYROMONAS GINGIVALIS
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1...1443
 US-09-221-017B-685

Alignment Scores:
 Pred. No.: 2,22e-79 Length: 1443
 Score: 743.00 Matches: 156
 Percent Similarity: 62.97% Conservative: 43
 Best Local Similarity: 49.37% Mismatches: 105
 Query Match: 43.48% Indels: 12
 DB: 4 Gaps: 5

US-10-005-429-25 (1-331) X US-09-221-017B-685 (1-1443)

Qy 12 ArgLeuGlySerGlyProAlaAlaHisThrAlaAlaIleValAlaAlaArg 31
 Db 1189 CGCTGTCTCATCATCGGTTCCGGACCTCCGGCTATACCGGCTATCTGCTCTCTG 1130
 Qy 32 AlaGluLeuValProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 51
 Db 1129 GCCAACCTCAACCCATCTCTACGAGG-----ATCAACCCGGCGGT 1085
 Qy 52 GlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMetGly 71
 Db 1084 CAGCTAACGACTACGACCGAGGTGGAACCTTCCGGGTATATCCGAAGGAATCACCGGT 1025
 Qy 72 AlaAspLeuMetAspAsnGlyArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSer 91
 Db 1024 ACGGAACGATGGAAGACCTGCGCAACAGCAACCGCTTCGGAGCGGACATCTGTCG 965
 Qy 92 GluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp---Ser 110
 Db 964 GGTATCGCTACAAAGCGGATTTGACGAGGCTCTTACAGGATCACGATAGACGGAGA 905
 Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGluHis 130
 Db 904 AAGGAATACAGCGGATGCTTATCTCCAGGCTGCGCAACAGCAACCTTACTTAGGC 845
 Qy 131 PheProGlySerAspAlaValTrpAsnArgGlyIleSerAlaCysAlaValCysAspGly 150
 Db 844 TTGGCCGATGAGCCAAATATCCGCGATGGTGTCTGCTGTGCTACCTGTGATGGA 785
 Qy 151 AlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMet 170
 Db 784 TTT-----TTCTATCGCAAGGAAGTAGCGGTAGTGGGGGAGGTGATCTGCTGTC 731
 Qy 171 GluGluSerAspPheLeuThrIlystIyGlySerHisValIleIleHisArgAsn 190
 Db 730 GAGGAGGCTCTCTATCTGGCATCGCTGGTGAACAGCTGCTACTGTGCTACGCAAGAAC 671

Qy 191 ThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnProLysIleLysVal 210
 Db 670 TATCTCGTCTCCAAAGGTATATGACGAGCGGTGATGAATACGCGCAACATAACCGTT 611
 Qy 211 LeuTrpAspSerGluValValGluAlaValGly-----GluAlaAsnGlyGlyProLeu 228
 Db 610 CTCTTGAACATAATATACCGTGGGTCTATTCCGGGAAACGGTGTGGAAGTGTCTATCTG 551
 Qy 229 AlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnValSerGly 248
 Db 550 -----GTGAACGCAAGAGAGAGCGGAGAGAGATGTTGACATGCGCATGTTGTT 497
 Qy 249 LeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeuGluLeu 268
 Db 496 TTTTCTCGCTATCGGTATACGCAACCTCGAAGATCTTCCGCCACTTACCTCGACTTG 437
 Qy 269 AspSerAspGlyTrpValGluThrLysProGlySerThrHisThrSerValLysGlyVal 288
 Db 436 GACGAAGTGGTTATATCTCGAGGAGGTTCGTCGCCGCGCACAAAGTTCCCGCGGTA 377
 Qy 289 PheAlaAlaGlyAspValGlnAspLysLysTrpArgGlnAlaIleThrAlaAlaGlySer 308
 Db 376 TTTGCTCGCGGCGAGCTTCCGACACACATATCGTCAGCTATCAGCGTCCGCGGATCA 317
 Qy 309 GlyCysMetAlaAlaLeuAspAlaGluHisTrpLeuGlnGluIleGly 324
 Db 316 GGTTCGAGGCTCTATCGAAGCAGAGCGTTATTTCGGCGGACCGGT 269

RESULT 11
 US-09-328-352-1552
 ; Sequence 1552, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 1552
 ; LENGTH: 963
 ; TYPE: DNA
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-1552

Alignment Scores:
 Pred. No.: 5.44e-76 Length: 963
 Score: 712.50 Matches: 247
 Percent Similarity: 64.49% Conservative: 60
 Best Local Similarity: 45.79% Mismatches: 95
 Query Match: 41.69% Indels: 19
 DB: 4 Gaps: 7

US-10-005-429-25 (1-331) X US-09-328-352-1552 (1-963)

Qy 11 ThrArgLeuCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleValAlaAla 30
 Db 31 TCTCGTTAATATATCTCGGTTCTGCGCTTATAGTGCAGCTGTATTATGCAAGCA 90
 Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
 Db 91 CGTCAATCTTAACCAACACACTTATTGCAAGT-----TTACAGCTTGGC 135
 Qy 51 GlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
 Db 136 GGCCCACTTACACACACACCGAAGTTGACAACTGGCGGCGGATCTCTGAAGTTTGA 195
 Qy 71 GlyAlaAspLeuMetAspAsnGlyArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
 Db 196 GGTCTGCGCTTAAATGAGCGGTATGCAAGCATCATCGCTTGGTACCAACTTGTCTC 255
 Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110

Db 463 TCCAGCTTACCTCTCTCCCGCCCTTCAAGATGTGGACGAGTGGACGAGTGGACGAA 522
Qy 108 AlaaspSerThrThrValLeuAlaAaspAlaValileValalaThrGlyAlaValalaArg 127
Db 523 GGCAGCGAGCGCGTCCGCGACCGCGCGCGTCTATCATTTGCCACGAGCGCGCAACGCGCGC 582
Qy 128 ArgLeuHisPheProGlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCysAlaVal 147
Db 583 CGTCTGACCTGCGCGCGAGGAGGAGCTTCTGCGAGACGAGATCAGCGCTGTGCGCTC 642
Qy 148 CysaspGlyAlaAlaProfilePheArgAsnLysProIleAlaValileGlyGlyGlyAsp 167
Db 643 TGCAGCGTGTGCGTGCCTATTTCCGTAACAAGCCCTGTACGTCTATGCGGTGTGTGAC 702
Qy 168 SerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIleHis 187
Db 703 TCCGCGCGCGAGGAGGAGGAGCTTCTGCGCAAGTACCGCAGCGAGCTGTCTCTGTT 762
Qy 188 ArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnProLys 207
Db 763 CGCAAGGACAGCTGCGTCTCTAATCATCATGCTGCTCTCTCTCTCTCTCTCTCTCTCT 822
Qy 208 IleLysValLeuTrpAspSerGluValValGluAlaTyrGly---GlyAlaAsnGlyGly 226
Db 823 TGCAGGTCGCGCTTCAACACCGCGTCCGCCACCGAGGTATTCGCGAGAACCAAGCCTAACCGC 882
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuAsnGlyGluValSerAspLeuGluVal 246
Db 883 CTATGACCCACCTTCGCTCAAGACGCTTCTCTAAGCGGAGGAGTCTGTGAGGCT 942
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 943 AACGGTCTCTTCTACGCTGTGTGTCACGACCGCCCGCAGTGTCTCTCTCTCTCTCTCT 1002
Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 1003 GAGCTCGACGACGAGGAGATCATCATCAACGCGCGGTACTAGCTTCACTAAGTGGAG 1062
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysTyrArgGlnAlaIleThrAlaAla 306
Db 1063 GGTGTTTTCGCTGCGGTGATGTTTCAAGATTAAGCGCTACCGTCAAGCTATCACAGTGC- 1121
Qy 306 ----- 306
Db 1122 CGGTATGTCATCTTCAAGATCTCATGTAGTAATTCGAATTTGGTAACTCAATATT 1181
Qy 307 -----GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGly 324
Db 1182 CTACAGGATCTGCTGTGTGCTGCTCTTGTAGGCTGAGAAATTCATCGCGAGACCGAG 1241
Qy 325 Ala---GlnGluGlyLys 329
Db 1242 ACTCACCAGGAGGCAAG 1259
RESULT 8
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
Alignment Scores:
Prob. No.: 2,59e-74 Length: 4403765
Score: 747.00 Matches: 164
Percent Similarity: 66.36% Conservative: 53
Best Local Similarity: 50.15% Mismatches: 95
Query Match: 43.71% Indels: 15
DB: 3 Gaps: 6
US-10-005-429-25 (1-331) x US-09-103-840A-2 (1-4403765)
Qy 8 ProLeuArgThrArg-IleCysIleIleGlySerGlyProAlaAlaHisThrAlaAla 27
Db 4393993 CCACCCGCTTCGCGAGCTGATCGTTATCGCTCCCGGCGGTACATCGCGCGCT 4394052
Qy 27 eTyrAlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAsp 47
Db 4394053 CTAAGCGCGCGCGCTGCGAGCTGCGCGCTGCTTTCGAGGCG-AC 4394097
Qy 47 eAlaAlaGlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAs 67
Db 4394098 GTCTTTTCGCGCGCGCTGATGACACCGACGCTGGAGAACTACCGCGGATTTCCGCA 4394157
Qy 67 nGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGly 87
Db 4394158 CGGATCATCCGCTCCAGAGTTGATGTAGATGCGGAGAACGCGCTGCGATTCGCGC 4394217
Qy 87 rAsnIleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArg- 105
Db 4394218 GGACCTTCGCTATGAGAGAGCTGCGATCATCTACCTTCACGGG-CCGCTGAAATCGGT 4394274
Qy 106 -ValSerAlaAspSerThrThrValLeuAlaAspAlaValileValalaThrGlyAla 125
Db 4394275 CGTACCGCGCGAGCGACAGACCCCGCGCGCGAGCGGATCTGCGATTCGCGCGC 4394334
Qy 125 lAlaArgAlaGluHisPheProGlySerAspAlaTyrTrpAsnArgGlyIleSerAla 145
Db 4394335 GGCACGCTATCTCAGCGTCCCGCGCAACAGGAATTTGTCGCGCGCGGTGAGTCTG 4394394
Qy 145 sAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValileGly 165
Db 4394395 CGCCACTTCGCGAGGATTC-----TTCCTCCGATCAGGACATCGCGCTATCGCGG 4394448
Qy 165 yGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyr 185
Db 4394449 CGGTGCTCGCAATGAGAGAGCTACCTTCCTGACCGGATTCGCTCGCAGTGTGAGCT 4394508
Qy 185 eIleHisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAs 205
Db 4394509 GGTGCTATCGCGCGAGTTCGCGGCTTCCAAAATCATGCTCGATCGCGCGCGCAACA 4394568
Qy 205 nProLysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaAsn 225
Db 4394569 CGACAGATACGTTCTCTACCAACACACCGCTGCTGCGCGGACCGGACACCA- 4394626
Qy 225 yGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeu 245
Db 4394627 -----GTGACCGGCTTTCGCGGTACCGACACCAACCGGTCGCCAAACCCCTGCC 4394679
Qy 245 nValSerGluPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGly 265
Db 4394680 GGTAACCGGTGTTTTCGCGATTCGCGCAGCGCGCGCTGCGGCTTGTGCGCGGAGC 4394739
Qy 265 nLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrS 285
Db 4394740 CATCGAGCTCGACCCGCGCGCTACGTTGTGTGCGAGGCGGTACCAACCGACCTCACT 4394799

167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleLeu 186
Db 366122 GATTCTGCTTAGAAGAGCTCTTACCTGACTGGTATGGAAGCCACCGTATATGTAGTT 366063
187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 366062 CATCGTAGAGATAAATCGGGCTTCTTAAGCTATGGAAGCTCGGCGCAAAACAATGAA 366003
207 LysIleLysValLeuThrPaspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
Db 366002 AAAATTACATTATTATGGAATAGCGAGATGTGTAATAATTCTGGAGATAGC----- 365952
227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 365951 ATTGTCCGTTCCGTAGATATTAGAAATGTTACACTCAAGAAATTACAACTAGAGAAGCT 365892
247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 365891 GCGGGGGTGTCTTCTGATAGCCATAGCCAAATACGATTTCTCGAGGACAGCTG 365832
267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 365831 ACCTTAGATGAGTCGGCTATATTGTGACTGAGAAAGGAAGCTCCCAAGACTTCTGTCCCT 365772
287 GlyValPheAlaAlaGlyAspValGlnAspLysTyrArgGlnAlaIleThrAlaAla 306
Db 365771 GGAGTATTGCTGCTGAGATGTTTCAGGATAAGTACTATCGTCAGCGGTTACTTCTGCA 365712
307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
Db 365711 GGAGTGGTGTGTATAGCAGCTAGATGCTGAAAGATTCTTA 365670

RESULT 7
US-08-386-729A-6
Sequence 6, Application US/08386729A
Patent No. 5753435
GENERAL INFORMATION:
APPLICANT: Aharonowitz, Yair
APPLICANT: Van Der Voort, Lucia H. M.
APPLICANT: Cohen, Gerald
APPLICANT: Bovenberg, Roelof A. L.
APPLICANT: Schreiber, Rachel
APPLICANT: Argaman, Anat
APPLICANT: Av-Gay, Yossef
APPLICANT: Nan, Helena M.
APPLICANT: Kattewilder, Alfred
APPLICANT: Pallisa, Harriet
TITLE OF INVENTION: An oxido reductase enzyme system
TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes
TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme
TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
TITLE OF INVENTION: production
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weill, Gotshal & Manges
STREET: 2882 Sand Hill Road, Ste. 280
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,729A
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/274,043
FILING DATE: 12-JULY-1994
APPLICATION NUMBER: US 07/820,688

FILING DATE: 24-MARCH-1992
APPLICATION NUMBER: PCT/NL91/000101
FILING DATE: 18-JUNE-1991
APPLICATION NUMBER: EP 90201598.1
FILING DATE: 18-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-024/020S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO. 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1423 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLSCULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Penicillium chrysogenum
FEATURE:
NAME/KEY: exon
LOCATION: 119...140
FEATURE:
NAME/KEY: intron
LOCATION: 141..223
FEATURE:
NAME/KEY: exon
LOCATION: 224..1123
FEATURE:
NAME/KEY: intron
LOCATION: 1124..1188
FEATURE:
NAME/KEY: exon
LOCATION: 1189..1271
FEATURE:
NAME/KEY: CDS
LOCATION: join(119..140, 224..1123, 1189..1271)
OTHER INFORMATION: /product= "HWM protein"
OTHER INFORMATION: /genes "trxB"
US-08-386-729A-6
Alignment Scores:
Pred. No.: 7,158-99 Length: 1423
Score: 905.00 Matches: 185
Percent Similarity: 69.36% Conservative: 55
Best Local Similarity: 53.47% Mismatches: 75
Query Match: 52.95% Indels: 32
DB: 1 Gaps: 4
US-10-005-429-25 (1-331) x US-08-386-729A-6 (1-1423)
QY 15 IleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeu 34
Db 223 GTTATTGGCTCGGGCCCTGGTGGCCACACTGCGGCTATCTATCTATCGCGCAGAGCTC 282
QY 35 LysProValLeuPheGluGlyTrpMetAlaAspIleAlaAlaGlyGlyGlnLeuThr 54
Db 283 CAGCCAGTCCCTTTACGAGGCGATGCTCGCCAAACGGTACCGCCGCGGTGGTCTCAGCTCAG 342
QY 55 ThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeu 74
Db 343 ACGACCACTGACGTGAGAACTTCCCGGATTCCCGAGCGGATCGCGCGCGCGAGCTC 402
QY 75 MetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrVal 94
Db 403 ATGGACAACATCGCGCCCAATCCGAGCGCTTCGGACCGGATCATCATCAGAGACCATC 462
QY 95 ThrAlaValAspPheSerAlaCysProPheArgVal-----Ser 107
Db 95 ThrAlaValAspPheSerAlaCysProPheArgVal-----Ser 107

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NAME/KEY: misc feature
LOCATION: (405001)..(420000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (420001)..(435000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc feature
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LOCATION: (720001)..(735000)
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (750001)..(765000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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LOCATION: (765001)..(780000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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LOCATION: (825001)..(840000)
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LOCATION: (840001)..(855000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (855001)..(870000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (870001)..(885000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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Alignment Scores:
Pred. No.: 3 83e-97 Length: 1230025
Score: 929.50 Matches: 176
Percent Similarity: 75.48% Conservative: 61
Best Local Similarity: 56.05% Mismatches: 70
Query Match: 54.39% Indels: 7
DB: 4 Gaps: 3
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US-10-005-429-25 (1-331) x US-09-198-452A-1 (1-1230025)

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Qy 9 LeuArgThrArgIleCysIlelleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr 28
Db 366596 ATTCATTCGGGTAAATATTATTTGTTTCCAGGTCCATCTGGATATACAGCGCAATTTAT 366537
Qy 29 AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAla 48
Db 366536 GCATCAAGAGCGCTTTTGATCTCTTTTATTTGAGGGGTTTCTCTGGG-----ATC 366483
Qy 49 AlaGlyGlyGlnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 68
Db 366482 TCTGTGGCCAGCTTATGACTACACAGAGTTGAGAAATTTCCAGGGTTTCTTGAAGGG 366423
Qy 69 IleMetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsn 88
Db 366422 ATTCTTGGGCGCAAACTTATGATATATATGAGAGCAGCGCTGTGGGTTTGGACCAAG 366363
Qy 89 IleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAla 108
Db 366362 ACACATGCTCAAGATATTATTTCCGTAGATTTTCTGTGCGCTTTTATTTTGAATCA 366303
Qy 109 AspSerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArg 128
Db 366302 AAAGAAGAAACCTATTCTTGTGATGCTGTATCATAGCTACAGAGCTTCTGCTAAACGT 366243
Qy 129 LeuHisPhePro-----GlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 366242 TTAGAAATTCCTGGAGCAGGAACAGATATTTGGCAAAAGAGTGAATCTGTGTGTGCC 366183
Qy 147 ValCysAspGlyAlaAlaProllePheArgAsnLysProIleAlaValIleGlyGlyGly 166
Db 366182 GTTTCGATGGGCTTCTCTATTTTAAAAATAAAGATCTTTATGTGTGATTTGGGGAGGG 366123
```

[illegible]

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; SEQ ID NO 24
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-598-747-24

Alignment Scores:
Pred. No.: 2,18-145 Length: 1021
Score: 1290.00 Matches: 251
Percent Similarity: 85.54% Conservatives: 27
Best Local Similarity: 77.23% Mismatches: 43
Query Match: 75.48% Indels: 4
DB: Gaps: 1

US-10-005-429-25 (1-331) x US-09-598-747-24 (1-1021)

Qy 11 ThrArgLeuCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 34 ACCGCGCTCTGATCGTTGGTTCGGCGCGCTGCCACACCGCGCATCTAGCGCGCC 93
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAaGly 50
Db 94 CGCCCGAGCTGAAGCGCTCTCTTGGAGGGCTGGATGGCCACACGACATCGCCCGGC 153
Qy 51 GlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 154 GCGCAGCTCACACACACCGACGCTGGAGAACTTCCCGGCTTCCGGAGGGCATCTTC 213
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 214 GCGGTGGAGCTGACCGCAAGTTCGCAAGCAGAGCGAGCGCTTCGGCACCCATCTTC 273
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 274 ACCGAGCCGTGACCAAGGTGACTTCTCGAGCAAGCGGTTCAAGCTCTTCACCGACTCC 333
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArgLeuHis 130
Db 334 AAGCCCATCTCGCGCAGCGCGGTATCTCCCACTCGCGCGCGCTGGCCAAAGTGGCTTCC 393
Qy 131 PheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 394 TTCTGGGCTTCGGCGAGGTCTCGCGCGCTCTGGAAACCGCGGCATCTCGGCTGCGCT 453
Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
Db 454 GTGTGCGACGCGCGCGCGCGATCTTCGCGCAACAGCGGCTCGCTGTGATCGTGGCGGA 513
Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
Db 514 GACAGCGCATGAGAGAGCGCAACTTCTCCACCAAGTACGAGTCCAGGTGTATCATC 573
Qy 187 HisArgArgAsnThrPheArgAlaSerIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 574 GACGCGCGCGCGCTTCGCGCGCTTCCCAAGATCATGACAGCAGCGCGCGCTCTCCAAACCG 633
Qy 207 LysIleLysValLeuTrpAsnSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
Db 634 AAGATCGACGTATCTCGACTCTCTCCGTGTGGAGGCTACGCGCAGCGCGCGCGGAC 693
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 694 GTGCTCGCGCGCTTCAAGGTGAAGAACGTGTGTGACCGCGCGAGTGTCTCCAGGTG 753
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 754 TCGCGCTCTCTTCGCGCATCGCGCACGAGCGCGCGCACCAAGTCTCTCGACGGCGCGGTG 813
Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 814 GAGCTGGACTCCGACGGCTACGTGGTGACCAAGCGCGCGCACCCACGACCTCCGTGCT 873
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
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874 GCGGTCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 933
307 GlySerGlyCysMethAlaLeuAspAlaGluHisTyrLeuGlnGlnGlyAlaGln 326
934 GGCACCGGTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 993
327 GluGlyLysSerAsp 331
994 CAGGCGCAAGTCCGAC 1008

RESULT 5
US-09-540-014-26
; Sequence 26, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del'Val, Greg
; APPLICANT: Calliau, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresoxin and
; FILE OF INVENTION: NADP-Thioresoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-540-014-26

Alignment Scores:
Pred. No.: 1,06e-136 Length: 998
Score: 1217.50 Matches: 244
Percent Similarity: 83.38% Conservatives: 27
Best Local Similarity: 75.08% Mismatches: 49
Query Match: 71.24% Indels: 6
DB: Gaps: 2

US-10-005-429-25 (1-331) x US-09-540-014-26 (1-998)

Qy 11 ThrArgLeuCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
Db 25 ACAAGGCTCTGTATCGTAGGAGTGGCCCGCGCGCGCACACCGCGCGGATTTACGAGCT 84
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAaGly 50
Db 85 AGGCTGAACCTTAACCTCTTCTTCGAAGGATGATGGCTAACGACATCGCTCCCGT 144
Qy 51 GlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 145 GGTCAACTCAACCAACACCGCGCT---GAGAAATTCGCCGATTTCCGAGAGGTATTCTC 201
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 202 GGAGTAGAGTCTACTGACAAATTCGTAACATCGGAGCGATTCGGTACTACGATATT 261
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 262 ACAGACGCGGTGACGAAAGTCGATTTCTCTCGAAACCGTTTAAAGCTATTTCACAGATTCA 321
Qy 311 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgA-gLeuHis 130
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Query Match: 88.36% Indels: 3
DB: 4 Gaps: 0

US-10-005-429-25 (1-331) x US-09-540-014-10 (1-995)

QY 1 MetGluGlySerAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
DB 1 ATGGAGGATCCG 60
QY 21 AlaAlaHisThrAlaAlaIleTyAlaAlaAlaAlaAlaAlaAlaAlaAla 40
DB 61 GCCGCGCACACG 120
QY 41 GlyTrpMetAlaAsnAspIleAlaAlaAlaAlaAlaAlaAlaAlaAla 60
DB 121 GGCTGGATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsn 80
DB 181 AACATCCCGGATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaVal 100
DB 241 CAGTCG 300
QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAla 120
DB 301 GCCCG 360
QY 121 AlaThrGlyAlaValAlaAlaArgLeuHisPheProGlySerAspAlaTy 140
DB 361 GCCCG 420
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsn 160
DB 421 GGCATCTCCG 480
QY 161 AlaValIleGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrTy 180
DB 481 GCCGTCATCG 540
QY 181 SerHisValTyIleIleHisArgGlnThrPheArgAlaSerLysIleMetG 200
DB 541 TCCCAAGTGTATCATCATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 201 ArgAlaLeuGluAsnProLysIleValLeuTrpAspSerGluValValGlu 220
DB 601 AGGCGCGCTCCATATCTAAGATCCAGGTTGTCTCGGACTC-GAGGTGTC 659
QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuAs 240
DB 660 GCGCGTGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluPro 260
DB 720 GGTCTGACCTTCAGGTGTCGCGCGCTTTCTTCGCGCATCGGCGCATGAG 779
QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyThrValGluThr 280
DB 780 TTTCTCAATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 839
QY 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLys 300
DB 840 ACACATACCATGTGTGA-GGGGTCTTTGCTGTGGAGAGGTGCAGGATAAG 898
QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu-AspAlaG 320
DB 899 CAGGCCATTACTCTCTCGATCAGGTTGATGGCTGCTTTGGGACCGCGGAC 958
QY 320 uGlnGluIleGlyAlaGluGluGlyLysSerasp 331
DB 959 GCAGGAGGTGGGTCACAGTGGGCAAGTCTGAT 992

RESULT 2
US-09-540-014-23
Sequence 23, Application US/09540014
Patent No. 5380372
GENERAL INFORMATION:
APPLICANT: Cho, Myeong-Je
APPLICANT: Del Val, Greg
APPLICANT: Caillaud, Maxime
APPLICANT: Lemaux, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Barley Gene for Thioresoxin and
TITLE OF INVENTION: NADP-Thioresoxin Reductase
FILE REFERENCE: 2001-0701.30
CURRENT APPLICATION NUMBER: US/09/540,014
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,739
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 995
TYPE: DNA
ORGANISM: Hordeum vulgare
US-09-540-014-23

Alignment Scores:
Pred. No.: 7,03e-172 Length: 995
Score: 1510.00 Matches: 302
Percent Similarity: 93.98% Conservative: 10
Best Local Similarity: 90.96% Mismatches: 19
Query Match: 88.36% Indels: 3
DB: 4 Gaps: 0

US-10-005-429-25 (1-331) x US-09-540-014-23 (1-995)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
DB 1 ATGGAGGATCCG 60
QY 21 AlaAlaHisThrAlaAlaIleTyAlaAlaAlaAlaAlaAlaAlaAlaAla 40
DB 61 GCCGCGCACACG 120
QY 41 GlyTrpMetAlaAsnAspIleAlaAlaAlaAlaAlaAlaAlaAlaAla 60
DB 121 GGCTGGATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsn 80
DB 181 AACATCCCGGATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaVal 100
DB 241 CAGTCG 300
QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAla 120
DB 301 GCCCG 360
QY 121 AlaThrGlyAlaValAlaAlaArgLeuHisPheProGlySerAspAlaTy 140
DB 361 GCCCG 420
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsn 160
DB 421 GGCATCTCCG 480

GenCore version 5.1.6
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Run on: May 5, 2004, 03:14:43 ; Search time 95.6061 Seconds
(without alignments)
1921.307 Million cell updates/sec

Title: US-10-005-429-25

Perfect score: 1709

Sequence: 1 MEGSAAPLRICIGSGP.....AALDAHYLQIGAGQEKSD 331

Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1510	88.4	995	US-09-540-014-10	Sequence 10, Appl
2	1510	88.4	995	US-09-540-014-23	Sequence 23, Appl
3	1478	86.5	1550	US-09-598-747-26	Sequence 26, Appl
4	1290	75.5	1021	US-09-598-747-24	Sequence 24, Appl
5	1217.5	71.2	998	US-09-540-014-26	Sequence 26, Appl
6	929.5	54.4	1230025	US-09-198-452A-1	Sequence 1, Appl
7	905	53.0	1423	US-08-386-729A-6	Sequence 6, Appl
8	747	43.7	4403765	US-09-103-840A-2	Sequence 2, Appl
9	747	43.7	4411529	US-09-103-840A-1	Sequence 1, Appl
10	743	43.5	1443	US-09-321-017B-685	Sequence 685, Appl
11	712.5	41.7	963	US-09-328-352-1552	Sequence 1552, Appl
12	709.5	41.5	49617	US-09-596-002-28	Sequence 28, Appl

13	709	41.5	1050	4	US-09-489-039A-4925	Sequence 4925, Ap
14	705	41.3	966	4	US-09-540-014-27	Sequence 27, Appl
15	703.5	41.2	954	4	US-09-328-352-3988	Sequence 3988, Ap
16	701	41.0	972	4	US-09-252-991A-13278	Sequence 13278, A
17	701	41.0	1413	4	US-09-252-991A-12680	Sequence 12680, A
18	700.5	41.0	1020	4	US-09-543-681A-1461	Sequence 1461, Ap
19	697	40.8	1830121	4	US-09-557-884-1	Sequence 1, Appli
20	697	40.8	1830121	4	US-09-643-990A-1	Sequence 1, Appli
21	600.5	35.1	640681	4	US-09-790-988-1	Sequence 1, Appli
22	549.5	32.2	933	4	US-09-134-000C-2109	Sequence 2109, Ap
23	538.5	31.5	13086	4	US-08-956-171E-16	Sequence 16, Appl
24	507.5	29.7	2412	4	US-08-961-527-62	Sequence 62, Appl
25	480	28.1	648	4	US-09-252-991A-15129	Sequence 15129, A
26	473	27.7	987	4	US-09-134-000C-492	Sequence 492, App
27	463	27.1	666	4	US-09-252-991A-14995	Sequence 14995, A
28	437	25.6	666	4	US-09-252-991A-14492	Sequence 14492, A
29	421.5	24.7	1517	4	US-09-543-681A-318	Sequence 318, App
30	397.5	23.3	1527	4	US-09-134-001C-1733	Sequence 1733, Ap
31	394.5	23.1	762	4	US-09-134-001C-2675	Sequence 2675, Ap
32	387.5	22.7	6252	4	US-08-956-171E-50	Sequence 50, Appl
33	382.5	22.4	1809	1	US-08-220-677A-1	Sequence 1, Appli
34	372.5	21.8	1539	4	US-09-107-532A-2905	Sequence 2905, Ap
35	372	21.8	580073	4	US-08-545-528D-1	Sequence 1, Appli
36	369.5	21.6	1572	4	US-09-328-352-2268	Sequence 2268, Ap
37	369.5	21.6	1572	4	US-09-328-352-2269	Sequence 2269, Ap
38	363.5	21.3	600	4	US-09-252-991A-14870	Sequence 14870, A
39	358	20.9	1664976	4	US-08-916-421B-1	Sequence 1, Appli
40	355.5	20.8	1569	4	US-09-252-991A-11892	Sequence 11892, A
41	355.5	20.8	2526	4	US-09-253-991A-12018	Sequence 12018, A
42	351.5	20.6	751	3	US-08-998-415-219	Sequence 219, App
43	351.5	20.6	1464	4	US-09-489-039A-5743	Sequence 5743, Ap
44	321	18.8	1575	4	US-09-540-236-786	Sequence 786, Appl
45	321	18.8	19619	4	US-09-596-002-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-540-014-10
; Sequence 10, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresoxin and
; TITLE OF INVENTION: NADP-Thioresoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-540-014-10
Alignment Scores:
Pred. No.: 7.03e-172 Length: 995
Score: 1510.00 Matches: 302
Percent Similarity: 93.98% Conservative: 10
Best Local Similarity: 90.96% Mismatches: 19

Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Alignment Scores:
Pred. No.: 920
Score: 1202.50
Percent Similarity: 87.71%
Best Local Similarity: 80.20%
Query Match: 70.36%
DB: 14

US-10-005-429-25 (1-331) x CK280506 (1-920)

Qy	9	LeuArgThrArgIleCysIlelleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr	28
Db	50	CTAAACCCGCTCTGTATCATCGGACGCCCGCGAGCTCATACGGCGCCATTAC	109
Qy	29	AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAla	48
Db	110	GCCGACGTCGCCGAGCTGAAGCGATTCCTTTGAAGGATGATGCTAACGACATAGCT	169
Qy	49	AlaGlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGly	68
Db	170	CCCGCGGTACGTTACGACACCGAGTGTGAGACTTCCCGGTTCCTCGAAGGT	229
Qy	69	IleMetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsn	88
Db	230	ATTGCGGTGTGTGAGCTATGGAAGCGTGCCTGCGGAGTCCGTTCGGGACACAA	289
Qy	89	IleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAla	108
Db	280	ATTCTACTGAACCTGTAACAAAGTGACTTTCTAAAGTCCCTTTGAGATGTTTCG	349
Qy	109	AspSerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArg	128
Db	350	TCTGATAGACTGTGCTAGCTGACGCGTATTGTTGCTACCGGTCTGTGCTAAGCG	409
Qy	129	LeuHisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCysAla	146
Db	410	CTTGACTTTCCCGGTCCGCAATGACGGTTCCTGGAATAGGGGAATTCGGCTTGTGCC	469
Qy	147	ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGly	166
Db	470	GTTTGTGACGGCGCGCTCCGATTTTAGGATAGCCATTGCGGTGATTGTTGGTGG	529
Qy	167	AspSerAlaMetGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIlelle	186
Db	530	GATTCAGCTATGGAAGAGCTAATTTTGTGACTAAATATGTTCTAAAGTGTATATT	589
Qy	187	HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro	206
Db	590	CATAGAGGATGAGTTTAGGCGATCGAAGATTTGCAAGTAGGACATTGATGATCCCT	649
Qy	207	LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyAlaAsnGlyGly	226
Db	650	AAATAGAGGTGATTTGGAACCTCAAGTGTAGTGGAGGCTTATGGGAGAG-----	700
Qy	227	ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal	246
Db	701	CTATTGGGTGGATGAAGGTGAAGATGTTGTTACTGGGGAAGTTTCGATTTCAGGTT	760
Qy	247	SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu	266
Db	761	TCGGTTCGTTTCGCCATTTGGCATGGAACCGCTACTAAGTTTTCGACGGCAGTTA	820
Qy	267	GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys	286
Db	821	GAGTTGGATTCTGATGGGTATGTTGTGACTAAGCCGGGACGACCTTCGACAGTGAAG	880

Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyr 299
Db 881 GGTGTGTTTCTGCTGTGTTGATGTGAGGATAGAAGTAT 919

RESULT 15

CK255109 995 bp mRNA linear EST 12-DEC-2003
LOCUS E57738746 potato callus cDNA library, normalized and full-length
DEFINITION Solanum tuberosum cDNA clone POC168 5' end, mRNA sequence.
ACCESSION CK255109
VERSION CK255109.1 GI:39811666
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
Other ESTs: E57738747
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers
1..995
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POC168"
/tissue_type="callus"
/lab_host="DH10B-Rona"
/clone_lib="potato callus cDNA library, normalized and
full-length"
/note="vector: pCWSport6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 3.22e-122 Length: 995
Score: 1202.50 Matches: 231
Percent Similarity: 88.04% Conservative: 34
Best Local Similarity: 76.74% Mismatches: 29
Query Match: 70.36% Indels: 7
DB: 14 Gaps: 2

US-10-005-429-25 (1-331) x CK255109 (1-995)

Qy	10	ArgThrArgIleCysIlelleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAla	29
Db	101	AAGACCAAGTTTGCATCATCGGAAGTGCACCGCGCTCACCGCGCCATTACGCA	160
Qy	30	AlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAla	49
Db	161	GCACGCGCGAGCTAAACACCGATCTTTTGAAGGATGATGGCAATGATATCGCGCA	220
Qy	50	GlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIle	69
Db	221	GTTGACAGCTCACACACCTCCGAGGTGAGATTTCCCGGTTTCCCGAAGGATC	280
Qy	70	MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle	89
Db	281	GCCTGTGGTGAACATCATGACCGGTCCGCTCAATCTGTTTCGATTCGGTACAGATC	340
Qy	90	LeuSerGluThrValThrAlaValAspPheSerAlaCysPropheArgValSerAlaAsp	109
Db	341	TTCACGTAACTGAAGTACGATTTCTCTGCTAGTCTCTTTCAAAGTCAATGTCGAT	400

/clone="P04C044"
 /tissue_type="abiotic stress treated leaf and root tissue"
 /lab_hosts="DH108-T0NA"
 /clone_lib="potato abiotic stress cDNA library"
 /note="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: Solanum tuberosum var. Kennebec plants were
 grown from cuttings on a 16hr light/8 hr dark cycle at 25
 C for 3-4 weeks. Abiotic stress conditions were applied to
 four separate sets of plants. Set 1 involved saturation of
 the soil with 150 mM NaCl and tissues were harvested at
 following application of the salt stress (leaves: 2hr,
 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
 Set 2 were grown under the standard conditions and then
 were water stressed by withdrawal of further watering
 applications. Drought stressed plants were harvested after
 cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
 and 5d). Set 3 were grown under the standard conditions
 and then were cold stressed by placement at 4 C. Cold
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 2d. Set 4 were grown under the standard conditions and
 then were heat stressed by placement at 35 C. Heat
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 2d and 4d and heat-stressed roots were harvested at 6 hr,
 12 hr, 1 d, and 4d. RNA was isolated from all tissues and
 equal RNA from each tissue and stress was pooled to
 construct the cDNA library. RNA sample."

ORIGIN

Alignment Scores:
 Pred. No.: 1,14e-122 Length: 981
 Score: 1206.50 Matches: 231
 Percent Similarity: 87.50% Conservative: 35
 Best Local Similarity: 75.99% Mismatches: 31
 Query Match: 70.60% Indels: 7
 DB: 14 Gaps: 2

US-10-005-429-25 (1-331) x CK270016 (1-981)

Qy 10 ArgThrArgIleCysIleGlySerGlyProAlaAlaHisThrAlaAlaIleGlyAla 29
 Db 79 AAGACCAAGATTGTCATCATCGAAGTGGACCGCGCTCACACCGCGCCANTTACGCA 138
 Qy 30 AlaArgAlaGluLeuLeuProValLeuPheGluGlyTrpMetAlaAsnAspIleAla 49
 Db 139 GCACGCGCGAGCTAAACCCATCTCTTTGAAGGATGGATGGCCAAATGATCGGCCA 198
 Qy 50 GlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIle 69
 Db 199 GGTGGACAGCTCACACCACTCCGAGGTTCAGAAATTCCTCCGGTTCCCGAAGGACTC 258
 Qy 70 MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle 89
 Db 259 GCCGTGTGTGAAGTCACTGACCGCGTGGCTGCTCAATCTGTTCGATTCGGTACCGAGTC 318
 Qy 90 LeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp 109
 Db 319 TTCAGTGAACGTGAAGTAAAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 378
 Qy 110 SerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgLeu 129
 Db 379 GAAGAGCTGTACTAGCAGAGCTGTATTATTCGCTATTCGCTATTCGCTATTCGCTAT 438
 Qy 130 HisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCys 145
 Db 439 GAATTCCTGATCCGGACGGCCAAATGATATTCGATATTCGCGGATCTCGCTGTGT 498
 Qy 146 AlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 165
 Db 499 GCTGTGTGTGACGGCGAGCTCCGATCTTCGTAACAAGCCCTTTCGCGGTGATCGTGTGT 558
 Qy 166 GlyAspSerAlaMetGluCysSerAsnPheLeuThrLysTyrGlySerHisValTyrIle 185

Db 559 GCGAGATTGCAATGCAAGAGCTACATTTCTGACCAAAATATGTTTGGAAAGTGTATATA 618
 Qy 186 ILeHisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsn 205
 Db 619 ATTCAATAGAGGATGAATTTAGGCTTCGAGATTATCGAAATAGGCAATGAGTAAC 678
 Qy 206 ProLysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaAsnGly 225
 Db 679 CCTAAGATAGAGTGAATTTGGAATTCCTGCTGCTGGTGGAGGCATATCGGAGAGTCT-- 735
 Qy 226 GlyProLeuAlaGlyValLysValLysValLysValLysValLysValLysValLys 245
 Db 736 -----TTGGGTGATTAAGGTGGAGAGTGGTTACTGGAGAGTATCAGATTTGGAG 789
 Qy 246 ValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGln 265
 Db 790 GTTTCGGTTGTTCTTTGCTATGTCGATGACCTGCTACCAATTTTGGATGGACAA 849
 Qy 266 LeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerVal 285
 Db 850 CTCAGTGTGATGCTGAGAGGATGTTGCAACCGTCCGAGGACGACAAAGACTAGCGIT 909
 Qy 286 LysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAla 305
 Db 910 AGAGGTGATTGCTGCTGCTGATGTCAGATAGAGTACCGGCGGACATCACTGCT 969
 Qy 306 AlaGlySerGly 309
 Db 970 GCTGTTCAGGA 981

RESULT 14
 CK280506
 LOCUS
 DEFINITION
 EST743228 Nicotiana benthamiana mixed tissue cDNA library,
 normalized, full-length Nicotiana benthamiana cDNA clone NEM109 5',
 end, mRNA sequence.
 CK280506
 VERSION
 CK280506.1 GI:39850125
 EST.
 KEYWORDS
 Nicotiana benthamiana
 ORGANISM
 Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Nicotiana.
 1 (bases 1 to 920)
 Buell, C.R., Hart, A., Zismann, V., Karanicheva, S.A., Day, B.,
 Staskiewicz, B., Jin, H. and Baker, B.
 Generation of EST sequences from Nicotiana benthamiana
 Unpublished (2003)
 Other ESTs: EST743227
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: CAG GAA ACA GCT ATG ACC.
 Location/Qualifiers
 1..920
 /organism="Nicotiana benthamiana"
 /mol_type="mRNA"
 /db_xref="taxon:4100"
 /clone="NEM109"
 /tissue_type="abiotic and biotic stress-treated leaves,
 callus tissue and root tissue"
 /lab_hosts="DH108-T0NA"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA
 library, normalized, full-length"
 /note="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: RNA was isolated from Nicotiana benthamiana
 tissues that include callus, roots from liquid culture
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;

FEATURES
source

EST751943 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBEM34 5', end, mRNA sequence.

CK289221.1 GI:39867503
 EST.
 Nicotiana benthamiana
 Nicotiana benthamiana
 Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 930)
 Buell, C.R., Hart, A., Zismann, V., Karameycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.
 Generation of EST sequences from Nicotiana benthamiana
 Unpublished (2003)
 Other ESTs: EST751944
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers
 1..930
 /organism="Nicotiana benthamiana"
 /mol_type="mRNA"
 /db_xref="taxon:4100"
 /clone="NBEM34"
 /tissue types="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
 /lab_host="DH10B-TonA"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length"
 /notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr, cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN
 Alignment Scores:
 Pred. No.: 1,77e-124 Length: 930
 Score: 1222.50 Matches: 239
 Percent Similarity: 88.18% Conservative: 22
 Best Local Similarity: 80.74% Mismatches: 30
 Query Match: 71.53% Indels: 5
 DB: 14 Gaps: 2

US-10-005-429-25 (1-331) x CK289221 (1-930)

Qy 9 LeuArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr 28
 Db 51 CTAARAACCCGCTCTGTATATCGGAGCGGCCCGCAGCTCATACGGCCGCAATTAC 110

Qy 29 AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAla 48
 Db 111 GCGGCACGTCGCGAGCTGAAGCCGATTCCTTTGAAGGATGGATGGCTACGACATAGCT 170

Qy 49 AlaGlyGlyGlnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 68
 Db 171 CCGCGCGGTCAGCTTACGACACACCGATGTGAGAACCTTCCCGGTTTCTCGAGGT 230

Qy 69 IleMetGlyAlaAspLeuMetAsnAsnCysArgAlaGlnSerLeuArgPheGlyThrAsn 88
 Db 231 ATTTGGCGGTGTGAGCTTATGGAACCGTGGCGTGGCGAGTCCGTTCTGTTCCGGACACAA 290

Qy 89 IleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAla 108
 Db 291 ATTCACTACTGAAGTGAATTAAGGTGACCTTTTCTAAAGTCCCTTTTGAGATTGTTGG 350

Qy 109 AspSerThrThrValLeuAlaAspAlaValIleValAlaThrGlyValAlaValaArgArg 128
 Db 351 TCTGATAGGACGTGCTAGCTGACCGCTTATTTGTTGCTACCGGTGCTGTGCTGAAGCG 410

Qy 129 LeuHisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
 Db 411 CTTGACTTTTCCCGCTCCGGCAATCAGCGGTTCTCGAATAGCGGAATTTCCGCTTGTGCC 470

Qy 147 ValCysAspGlyAlaAlaAlaPheGlyPheArgAlaValProIleAlaValIleGlyGly 166
 Db 471 GTTGTGACGGCGCGCTCCCGATTTTAGGATAAGCCATTGCGCGTGTATTGGTGGGG 530

Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
 Db 531 GATTCAGCTATCGAAGAGCTAATTTTGTGACTAAATATGTTCTAAAGTGTATATTAT 590

Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
 Db 591 CATAGAGGGATGAGTTTAGCGCATCGAAGATTATGCAAAAGTAGAGCATGAGTAACCT 550

Qy 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
 Db 651 AAAATAGAGTGATTTGGAACTCAAGTGTAGTGGAGGCTTATGGGAGAG----- 701

Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
 Db 702 CTATTGGGTGGATGAAGGTGAAGATGTTGTACTCGGGGAAGTTTCGGATTTCAGGTT 761

Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
 Db 762 TCGGTTTGTGTTTCCCATTCGGCATGACCGCTACTTAAGTTTTCGACGGGCAAGTTA 821

Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
 Db 822 GAGTTGGATTCTGATGGGTATGTTGTGACTAAGCCGGGAGCCAGCTTGACCAAGTGTAA 881

Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAla 302
 Db 882 GGTGTGTTTGTCTGCTGATGTGACGAGTAAAGATATAGGCAAGCT 929

RESULT 13
 CK270016
 LOCUS
 DEFINITION EST716094 potato abiotic stress cDNA library Solanum tuberosum cDNA clone FOACQ44 5' end, mRNA sequence.

ACCESSION CK270016
 VERSION CK270016.1 GI:39826994
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 981)
 Buell, C.R., Hart, A., Zismann, V., Karameycheva, S.A. and Baker, B.
 Generation of ESTs from abiotic stressed potato tissue
 Unpublished (2003)
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers
 1..981
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"

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Qy 186 ILeHsArgArgAnThrPheArgAlaSerlySileMetGlnAlaAaGAlaLeuGluAun 205
Db 573 ATTCATAGGAGGAGTAATTTAGGCGCTTCGAGGATTATCGCAATATAGCGCATTCGAGTAAC 632
Qy 206 ProlySileLySValLeuTriPAspSerGluValValGluAlaTyrGlyGlyAlaAsnGly 225
Db 633 CCTAAGATAGAGGTGATTTCGAATTCCTGCTGTGTGGAGGCATATGGGGAGAACTCT--- 689
Qy 226 GlyProLeuAlaGlyValLySValLySAsnLeuLeuAsnGlyGluValSerAspLeuGln 245
Db 690 -----TTGGGTGGATTAAAGGTGGAGATGTGTTACTCGAGAGGTATCAGATTGGAG 743
Qy 246 ValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLySValPheLeuGlyGlyGln 265
Db 744 GTTTCGGGTTTGTCTTGTCTATTGGGATGAACCTGCTACCAATTTTGGATGGACAA 803
Qy 266 LeuGluLeuAspSerAspGlyTyrValGluThrLySProGlySerThrHisThrSerVal 285
Db 804 CTGCAGTTGGATGCTGAGAGGTATGTTGCAACCGTGCAGGGGACGACAAAGACTAGCGTT 863
Qy 286 LysGlyValPheAlaAlaGlyAspValGlnAspLySValTyrArgGlnAlaIleThrAla 305
Db 864 AGAGGTGATTGCTGCTGGTGATGTGCAGATAGAGTACCGGCAAGCCATCACTGCT 923
Qy 306 AlaGlySerGlyCysMetAla 312
Db 924 GCTGTTCCAGATGATGGCA 944

RESULT 11
CK252016 943 bp mRNA linear EST 12-DEC-2003
LOCUS EST735653 potato callus cDNA library, normalized and full-length
DEFINITION Solanum tuberosum cDNA clone POBR95 5' end, mRNA sequence.
ACCESSION CK252016
VERSION CK252016.1 GI:39805600
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
REFERENCE Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
1 (bases 1 to 943)
AUTHORS Generation of ESTs from potato callus tissue
TITLE Unpublished (2003)
JOURNAL Other ESTs: EST735654
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: Art TAG GTG ACA CTA TAG.

FEATURES
Location/Qualifiers
1..943
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POBR95"
/tissue_type="callus"
/lab_host="DH10B-TonA"
/clone_lib="potato callus cDNA library, normalized and full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

ORIGIN
Alignment Scores:
Pred. No.: 6,55e-126 Length: 943
Score: 1235.50 Matches: 236
Percent Similarity: 88.24% Conservative: 34

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Best Local Similarity: 77.12% Mismatches: 29
Query Match: 72.29% Indels: 7
DB: 14 Gaps: 2
US-10-005-429-25 (1-331) x CK252016 (1-943)
Qy 10 ArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaIleTyrAla 29
Db 35 AAGACAAAGATTTCATCATCGGAAGTGGACCGCGCTCACACCCGCGCAITTCGCA 94
Qy 30 AlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAla 49
Db 95 GCACGCGCGCGAGCTAAACCGATCCCTTTTGAAGATGGATGCCCAATGATATCGGCCA 154
Qy 50 GlyGlyGlnLeuThrThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIle 69
Db 155 GGTGGACAGCTCAACACCCCTCCGAGGTTCGAAATTTCCCGGTTCCCGGAAGGACTC 214
Qy 70 MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle 89
Db 215 GCGGTGGTGAATCTCATGGACCGGTGCCGTGCTCAATCTGTTGATTCGGTACACAGATC 274
Qy 90 LeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp 109
Db 275 TTCACGTGAACTGTAAAGTAACGTTGATTTCTCTGCTAGTCTCTTCAAAGTCATGTCGAT 334
Qy 110 SerThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaAlaArgArgLeu 129
Db 335 GAAAGGACTGTACTAGCAGACGCTGTTATTATTCGTACTGCTGCTGTTGCGAAGCGGCT 394
Qy 130 HisPheProGlySer-----AspAlaTyrTyrAsnArgGlyIleSerAlaCys 145
Db 395 GAATTTCTCGATCCGCGACGCGCAAGTGAATTCGCGGATCTCGGCTGT 454
Qy 146 AlaValCysAspGlyAlaAlaProllePheArgAsnLysProIleAlaValIleGlyGly 165
Db 455 GCTGTGTGTGACGCGCAGCTCCGATCTTTTCGTAACAAGCCTTTGGCGGTGATCGGTGT 514
Qy 166 GlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIle 185
Db 515 GGAGATTTCAGCATGGAGAGCTACATTTCTACGCAATATGTTTCGAAAGTGATATA 574
Qy 186 IleHisArgArgAnThrPheArgAlaSerLySileMetGlnAlaAlaLeuGluAun 205
Db 575 ATTCATAGGAGGATGAATTTAGGCGCTTCGAGATTATGCAATATGCGAATAGGCGATTCAGTAAC 634
Qy 206 ProlySileLySValLeuTriPAspSerGluValValGluAlaTyrGlyGlyAlaAsnGly 225
Db 635 CCTAAGATAGAGGTGATTTCGAATTCCTGCTGTGTGGAGGCATATGGGGAGAACTCT--- 691
Qy 226 GlyProLeuAlaGlyValLySValLySAsnLeuLeuAsnGlyGluValSerAspLeuGln 245
Db 692 -----TTGGGTGGATTAAAGGTGGAGATGTGTTACTCGAGAGGTATCAGATTTGGAG 745
Qy 246 ValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLySValPheLeuGlyGln 265
Db 746 GTTTCGGGTTTGTCTTGTCTATTGGGATGAACCTGCTACCAATTTTGGATGGACAA 805
Qy 266 LeuGluLeuAspSerAspGlyTyrValGluThrLySProGlySerThrHisThrSerVal 285
Db 806 CTGCGTTGGATGCTGAGAGGTATGTTGCAACCGTGCAGGGGACGACAAAGACTAGCGTT 865
Qy 286 LysGlyValPheAlaAlaGlyAspValGlnAspLySValTyrArgGlnAlaIleThrAla 305
Db 866 AGAGGTGATTGCTGCTGGTGATGTGCAAGATAAGAAGTACCGGCAAGCCATCACTGCT 925
Qy 306 AlaGlySerGlyCysMet 311
Db 926 GCTGTTCCAGATGATG 943

RESULT 12
CK289221
LOCUS CK289221 930 bp mRNA linear EST 15-DEC-2003

```

QY	30	AlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAa	49
Db	125	GCACGCGCGAGCTAAACCGATCTTTTGAAGGATGATGCCAATGATATCGGCCA	184
QY	50	GlyGlyGlnLeuThrThrAspValGluAsnProGlyPheProAsnGlyIle	69
Db	185	GGTGGACAGCTCAACACCTCCGAGGTGAGAAATTCCTCCGAGGAGACTC	244
QY	70	MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle	89
Db	245	GCCGGTGGTGAATCATGACCGCGTCCGCTCAATCTGTCATTCGTTCCGTACACAGATC	304
QY	90	LeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp	109
Db	305	TTCACTGAACCTGTAGTACCTGATTTCTCTGCCAGTCTTTCAAAGTCATGTCGGAT	364
QY	110	SerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGlu	129
Db	365	GAAGGACTGTACTAGACACACTGTATTATTCGTACTGTCTGTTCGCAAGCGCTT	424
QY	130	HisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCys	145
Db	425	GAATTTCTCTGGATCCGCGCAGCGCAATGATATTTGGAAATCGCGGATCTCGGCTGC	484
QY	146	AlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly	165
Db	485	GCTGTGTGTGACGCGCAGCTCCGACTTCGTACAGCTTTGCGGCTGATCGGTGT	544
QY	166	GlyAspSerAlaMetGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIle	185
Db	545	GGAGATTCAGCAATGGAAGAAGCTACATCTTTCTCAGCAATATGTTTCAAAAGTGTATATA	604
QY	186	IleHisArgGlnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsn	205
Db	605	ATTCTAGAAGAGATGAATTTAGGCTTCGAAATATGCGAATAGGCGATTCAGTAC	664
QY	206	ProLysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyAlaAsnGly	225
Db	665	CCTAAGATAGAGGTGATTTGGAATCTGCTGTGGTGGAGCATATGGGGAGATCT--	721
QY	226	GlyProLeuAlaGlyValLysValLysAsnLeuAsnGlyGluValSerAspLeuGln	245
Db	722	-----TTGGTGTGATTAAGGTGGAGATGTTGGTACTGAGAGGTATCAGATTTGGAG	775
QY	246	ValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGln	265
Db	776	GTTCGGGTTTGTCTTTGCTATTTGGCATGAACCTGCTACCAATTTTGGATGACAA	835
QY	266	LeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerVal	285
Db	836	CTGCAGTTGGATGCTGAGAGGTATGTTCAACCGTCCAGGACGACAAAGACTAGCGTA	895
QY	286	LysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAla	305
Db	896	AGAGGTGATTTGCTGCTGTGATGTCAGATAGAGATACCGGACAGCCATCTGCT	955
QY	306	AlaGlySerGlyCysMetAlaAlaLeuAspAlaGlu	317
Db	956	GCTGGTTCAGATGCATGGCAGCGTTGGATGCAGAG	991
RESULT 10			
CK258706			
LOCUS			
DEFINITION			
EST742343 potato callus cDNA library, normalized and full-length			
Solanum tuberosum cDNA clone POCDF49 5' end, mRNA sequence.			
ACCESSION			
CK258706			
VERSION			
CK258706.1 GI:39815686			
KEYWORDS			
EST.			
SOURCE			
Solanum tuberosum (potato)			
ORGANISM			
Solanum tuberosum			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			

asterids; lamids; Solanales; Solanaceae; Solanum.			
1 (bases 1 to 946)			
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.			
Generation of ESTs from potato callus tissue			
Unpublished (2003)			
Other ESTs: EST742344			
Contact: Robin Buell			
The Institute for Genomic Research			
9712 Medical Center Dr, Rockville, MD 20850, USA			
Email: potato-array@tigr.org			
Clones can be requested from TIGR via potato@tigr.org			
Seq primer: ATT TAG GTG ACA CTA TAG.			
Location/Qualifiers			
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/organism="Solanum tuberosum"			
/mol_type="mRNA"			
/cultivar="Kennebec"			
/db_xref="taxon:4113"			
/clone="POCDF49"			
/tissue_type="callus"			
/lab_host="DH10B-TonA"			
/clone_lib="potato callus cDNA library, normalized and			
full_length"			
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;			
supplier: RNA was isolated from Solanum tuberosum var.			
Kennebec callus tissue grown on solid media."			
ORIGIN			
Alignment Scores:			
Pred. No.: 2,378-126 Length: 946			
Score: 1239.50 Matches: 237			
Percent Similarity: 88.27% Conservative: 34			
Best Local Similarity: 77.20% Mismatches: 29			
Query Match: 72.53% Indels: 7			
DB: 14 Gaps: 2			
US-10-005-429-25 (1-331) x CK258706 (1-946)			
QY	10	ArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaIleTyrAla	29
Db	33	AAAGCAAAGTTGCAATCATCTCGAAGTGCAGCGGCGCTCACACCGCCGCCATTTACGCA	92
QY	30	AlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAa	49
Db	93	GCACGCGCGAGCTAAACCGATCTTTTGAAGATGATGCGCAATGATATCGGCCCA	152
QY	50	GlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIle	69
Db	153	GGTGGACAGCTCACACCACTCCGAGGTGAGAAATTTCCCGGTTTCCGGAAGACTC	212
QY	70	MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle	89
Db	213	GCGGTGGTGAATCATCTGACCGGTCCGCTGCTCAATCTGTTGATTCGGTACACAGATC	272
QY	90	LeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAsp	109
Db	273	TTCACTGAACCTGTAAGTAACGTTGATTTCTCTGCTAGTCTTTCAAAGTCATGTCGAT	332
QY	110	SerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGlu	129
Db	333	GAAGGACTGTACTAGCAGCGCTGTTATTATCGCTACTGCTGCTGCTGCTGCTGCTGCT	392
QY	130	HisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCys	145
Db	393	GAATTTCTCTGGATCCGCGCAGCGCAATGATATTTGAAATCGCGGATCTCGGCTGT	452
QY	146	AlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly	165
Db	453	GCTGTGTGACGCGCGAGCTCCGATCTTTTCGTAACAGCCCTTTGGCGGTGATCGGTGT	512
QY	166	GlyAspSerAlaMetGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIle	185
Db	513	GGAGATTCAGCAATGGAAGAAGCTACATTTCTGACGCAATATGTTTCGAAAGTGTATATA	572

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source

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1..970
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POA8690"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="PH108-Tona"
/clone_lib="potato abiotic stress cDNA library"
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, 1d,
and 4d). Set 2 were grown under the standard conditions and
then were cold stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

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ORIGIN

```

Alignment Scores:
Pred. No.: 6 99e-129 Length: 970
Score: 1262.50 Matches: 249
Percent Similarity: 88.10% Conservative: 25
Best Local Similarity: 80.06% Mismatches: 31
Query Match: 73.87% Indels: 6
DB: 14 Gaps: 2

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US-10-005-429-25 (1-331) x CK278595 (1-970)

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QY 9 LeuArgThrArgIleCysIlelleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr 28
DB 49 CTAAAAAATAGCGTTTGTATAATCGGAGTGGCCCTGCAGCTCACACAGTGCATTTAC 108
QY 29 AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAla 48
DB 109 GCAGCCGCGCGGAGCTTGAGCCGATCTTTTCAGAGATGGATGATGATGATGATGATGAT 168
QY 49 AlaGlyGlyGlnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 69
DB 169 CCGCGGGTCCAGCTTACGACCCACACAGATGTTGAGATTTTCTGCTTTCCTCCCGAAGGT 228
QY 69 IleMetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsn 88
DB 229 ATTGGCGCGCGGAGCTTATGAAAAAGTGTGGGCGAGTCTGTTGTTTGGGACACAA 288
QY 89 IleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAla 108
DB 289 ATTATACTACAAACGGTAACTAAGTTGATTTTCTAAAAAGTCTTTTAAAGTTGTTTCT 348
QY 109 AspSerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArg 128

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DB 349 GATGATAGGACTGTATTAGCTGACGCCGCTTATTCTCGCTACTGGTCTGTGGCTAAGAGG 408
QY 129 LeuHisPheProGlySer-----AspAlaTyrTTPAsuAlaGlyIleSerAlaCysAla 146
DB 409 CTTGAATTCCTCCGCTCCGCAATAATCGCTTCTCGAATAAGGGATATCAGCTTGGCC 468
QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
DB 469 GTTCTGATGTTGCTGCTCCCGATATTCCGTAATAAGCCATTAGCTGTAAATGTGGTGA 528
QY 167 AspSerAlaMetGluLysSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
DB 529 GATTCCTGCTAGGAAGAAGCTAAATTTTAACTAATAATGTTTCGAAAGTGTATATTATT 588
QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
DB 589 CATAGGAGGATGAATTTAGGGCATTCGAAGATAATGCAAAATAGGCCATTAGTAACCT 648
QY 207 LysIleLysValLeuTyrAspSerGluValValGluAlaTyrGlyAlaAsnGlyGly 226
DB 649 AAAATAGAGGTGATTGGAAATTTCTACTAGTGGAGGCTTATGGGGAAG----- 699
QY 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
DB 700 CTTTGGGTGGATTGCAAGTGAATAATTTCTACAGAGAGATTTCTGATTGAATGTT 759
QY 247 SerGlyLeuPhePheAlaIleHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
DB 760 TCAGGCTTTGTTTTCGCCAATTCGACCAACGACCAAGCTTTTGGTAAGCAATTA 819
QY 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
DB 820 GAGTTGGATTCGATGGATTTGTTGTAAGTCGCGGAGGACGACACTGACCACTGTAGG 879
QY 287 -GlyValPheAlaAlaGlyAspValGlnAspLysTyrArgGlnAlaIleThrAlaAla 306
DB 880 GGCTGTTTGTCTGCTGCTGATGTCAGGATAAGAAGTAGGCAAGCTATTACTGCTGC 939
QY 306 aclySerGlyCysMetAlaAlaLeuAspAla 316
DB 940 TGGCTCAGGGTGCATGGCGGCTTTGGATGCT 970

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RESULT 8
CK286466 947 bp mRNA linear EST 15-DEC-2003
LOCUS EST749188 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBME229 5'
end, mRNA sequence.
ACCESSION CK286466
VERSION CK286466.1 GI:39862056
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 947)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST749189
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

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FEATURES

source

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1..947
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"

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307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHis 318
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944 GGCTCAGGGTGATGGCGAGCTTATAGATCCCGAAT 979

RESULT 6
CK289722
LOCUS EST752444 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NMBP82 5',
end, mRNA sequence.
ACCESSION CK289722
VERSION CK289722.1 GI:39868489
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 976)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST752445
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
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            /organism="Nicotiana benthamiana"
            /mol_type="mRNA"
            /db_xref="taxon:4100"
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            /tissue_type="abiotic and biotic stress-treated leaves,
            callus tissue and root tissue"
            /lab_host="DH10B-TonA"
            /clone_lib="Nicotiana benthamiana mixed tissue cDNA
            library, normalized, full-length"
            /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
            supplier: RNA was isolated from Nicotiana benthamiana
            tissues that include callus, roots from liquid culture
            grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
            cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
            challenged leaves (Pseudomonas syringae pv tomato 12 hr;
            Xanthomonas campestris pv campestris 12 hr, 18hr;
            Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
            campestris pv vesicatoria 18hr). RNA was isolated from
            these tissues and pooled in approximately equal molar
            amounts."

ORIGIN
Alignment Scores:
Pred. No.: 1,976-129 Length: 976
Score: 1267.50 Matches: 249
Percent Similarity: 88.39% Conservative: 25
Best Local Similarity: 80.3% Mismatches: 30
Query Match: 74.1% Indels: 6
DB: 14 Gaps: 2

US-10-005-429-25 (1-331) x CK289722 (1-976)

Qy 9 leuArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr 28
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Db 56 CTTAAACCCCGCTCTGATCATCTGCGACGCGCGCGAGCTCATACAGCGCCATTAC 115

Qy 29 AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAla 48
|||||
Db 116 GCGGACGTCGCCAGCTAAAGCGGATCTCTTTGAAGGATGATGGCTAACGACATAGT 175

Qy 49 AlaGlyGlyGlnLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 68
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Db 176 CCCGGTGGTCACTACGACCACCCGACGTCGAGAACTTTCCCGGTTTCCCTGAGGT 235
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Qy 69 IleMetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsn 88
|||||
Db 236 ATTGGCGGTGGTGAAGTATGGACCGTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 295
|||||
Qy 89 IleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAla 108
|||||
Db 296 ATTCACTACTGAACCTGTAACCTGTAACCTGTAACCTGTAACCTGTAACCTGTAACCT 355
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Qy 109 AspSerThrThrValLeuAlaAspAlaValIleValAlaAlaThrGlyAlaValAlaArg 128
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Db 356 TCTGATAGGACTGTGTAGCTGAGCGCTCATTTGTTGCTACCGTCTGTAGCTAAGCG 415
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Qy 129 LeuHisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
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Db 416 CTTGAATTTCCCGGCTCCGCAATGACGGGTCTCGAATAGGGGAATTTCCGGTTGTGCC 475
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Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
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Db 476 GTTTGTGACGTCGCGCTCCGATTTTTCGATTTTTCGATTTTTCGATTTTTCGATTTTTC 535
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Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysThrLysThrLysThrLysThrLys 186
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Qy 187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
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Db 596 CATAGGAGGATGAGTTAGGGCTATCCAGATTTATGCAATAGTAGAGCATTTGAGTAACCT 655
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Qy 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
|||||
Db 656 AATATAGAGTGTATTTGGAACTCAAGTGTAGTGGAGCTTATGGGAGAGAG----- 706
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Qy 227 ProLeuAlaGlyValLysValLysAsnLeuAsnGlyGluValSerAspLeuGlnVal 246
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Db 707 CTATTGGTGGTATGAAAGTGAAGATTTGTTTCTGCGGCAAGTTTCGATTTTCGAGTTT 766
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Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
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Db 767 TCGGTTTGTGTTTTCGCACTGGCATGACCACTACTAAGTTTTCGATTTTCGAGTTT 826
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Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerVal-Ly 286
|||||
Db 827 GAATTCGATTCGATGCGTATGTTGACTAATCCGGGAACGACGTTGACGAGTTTGTAG 886
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Qy 286 sGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAl 306
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Db 887 GGGGTGTTTTCGCTGCTGATGTGCGAGTAAAGATACAGGACAGCTATTACAGCTGC 946
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Qy 306 aGlySerGlyCysMetAlaAlaLeuAsp 315
|||||
Db 947 TGGTTCAGGCTGCATGGCAGCTTAGAT 974
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RESULT 7
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LOCUS EST724663 potato abiotic stress cDNA library Solanum tuberosum cDNA
DEFINITION clone POAE690 5' end, mRNA sequence.
ACCESSION CK278585
VERSION CK278585.1 GI:39835563
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 970)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST724664

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Db 543 AGGAGGGATGAGTTTGGGCGATCCAGAGATTATGCAAAAGTAGACGATTGTAACCCCTAAA 602
Qy 208 IleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaSerGlyGlyPro 227
Db 603 ATAGAGTGGATTGGAACTCAAGTGTAGTGGAGCTTATGGGAGAG-----CTA 653
Qy 228 LeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnValSer 247
Db 654 TTGGTGGGATTGAAGTGAAGAAATGTTTACTCGGCAAGTTTCGGATTTCGAGGTTTCG 713
Qy 248 GlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeuGlu 267
Db 714 GGTGTGTTTTCCCGATGGCGATGAGACCGAGCTACTAGTTTGTGATGGCGAGTAGAA 773
Qy 268 LeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLysGly 287
Db 774 TTGGATTCTGATGCTATGTTGTGACTAATCCGGGAACGAGCTTGACCAAGTGTAGGGGT 833
Qy 288 ValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAlaGly 307
Db 834 GTGTTTGTCTGCTGCTGATGTCGAGGATAAGAGTACAGGCAAGCTATTACAGCTGCTGCT 893
Qy 308 SerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLysLeuGlnLutIleGly 324
Db 894 TCAGGGTGATGCGACGCTTTAGATGCGACATCTTGCAGAAATTTGTT 944

RESULT 5
LOCUS CK283459
DEFINITION Nicotiana benthamiana mixed tissue cDNA library.
normalized, full-length Nicotiana benthamiana cDNA clone NEMAH16 5'
end, mRNA sequence.
ACCESSION CK283459
VERSION 1 GI:39856092
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
AUTHORS Staskawicz, B., Jin, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST746182
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES
source
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/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NEMAH16"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TONa"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves [Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr]. RNA was isolated from
these tissues and pooled in approximately equal molar

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amounts."
ORIGIN
Alignment Scores:
Pred. No.: 1,58e-133 Length: 981
Score: 1304.50 Matches: 255
Percent Similarity: 88.78% Conservatives: 22
Best Local Similarity: 81.73% Mismatches: 30
Query Match: 76.33% Indels: 5
DB: 14 Gaps: 2
US-10-005-429-25 (1-331) x CK283459 (1-981)
Qy 9 LeuArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr 28
Db 53 CTAATAAACCGCTCTGTATCATCGCGCGCCCGCAGCTCATACGCCGCCCAATTTAC 112
Qy 29 AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAla 48
Db 113 GCCGCAGCTGCCGAGCTGAAGCCGATCTCTTTGAGGATGGATGCTAACGACATAGCT 172
Qy 49 AlaGlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGly 68
Db 173 CCCGGCGGTACGTTACGACCAACCGATGTCGAGAACTTTCCCGGTTTCTCTGAAGGT 232
Qy 69 IleMetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsn 88
Db 233 ATTGGCGGTGGTGGAGCTATGGAACGGTCCCGTGCAGTCCGTTCTTTCCGGACACA 292
Qy 89 IleLeuSerGlyThrValThrAlaValAspPheSerAlaCysPropheArgValSerAla 108
Db 293 ATTACATGAACTGTAACCTAAAGTGACTTTTCTAAAAGTCCTTTTCAGATTGTTTGG 352
Qy 109 AspSerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgAs 128
Db 353 TCTGATAGAGCTGTCTAGCTGACCGCGTTATTTGTGTACCGGTGCTGTGCGTAAGCGG 412
Qy 129 LeuHisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 413 CTTGACTTTCCCGGCTCCGGCAATGACGGGTTCTGNAATAGGGAATTTTCGGCTTGTGCC 472
Qy 147 ValCysAspGlyAlaAlaProllePheArgAsnLysProIleAlaValIleGlyGly 166
Db 473 GTTGTGAGCGGCGCGCTCCGATTTTATAGGAATAAGCCCATTCGCGGTGATTGTTGGTGG 532
Qy 167 AspSerAlaMetGluLysSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
Db 533 GATTACGCTATGCAAGAGCTAATTTTGTACTAATATGTTCTTAAGTGTATATTAT 592
Qy 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaAlaArgAlaLeuGluAsnPro 206
Db 593 CATAGAGGGATGAGTTTAGGGCATCGAAGATTATGCAAAAGTAGAGCATTTGAGTAACCT 652
Qy 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
Db 653 AAAATAGAGGTGATTGTGGAACCTCAAGTGTAGTGGAGGCTTATGGGAGAGAG----- 703
Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 704 CTAATTGGGTGGATTGAGGTGAAGATGTTGTACTGGGGAAGTTTCGGATTTCAGGTT 763
Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 764 TCGGGTTTGTGTTTTCGCCATGCGCATGAACCCGCTACTAAGTTTTTTGACCGGCGAGTTA 823
Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 824 GAGTTGGATTCTGATGGGTATGTTGTGACTAAGCCGGGAGACCTCTTGACCGAGTGTAA 883
Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
Db 884 GGTGTGTTTGTCTGCTGCTGATGTCAGGATAGAAGTATAGGCAAGCTATTACAGTGTCT 943

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QY 89 IleLeuSerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAla 108
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QY 109 AspSerThrValLeuAlaAspAlaValIleValAlaThrGluValAlaArgArg 128
Db 348 TCTGATAGACTGCTAGCTGACCCCTATTGTTGCTACCGGTCTGTGGCTAAGCGG 407
QY 129 LeuHisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 408 CTTGACTTTCGGCGCTCGGCAATGACGGTTTCTGGAATAGGGGAATTCGGCTGTGTC 467
QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGly 166
Db 468 GTTTGTGACGGCGCGCTCCGATTTTAGGAATAGCCATTGGCGGTGATTGGTGGG 527
QY 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
Db 528 GATTTCAGCTATGGAAGAAGCTAAATTTTGTGCTAAATATGTTCTAAAGTGTATATTAT 587
QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 588 CATAGAGGGATGAGTTTAGGCGATCGAAGATTATGCAAGTAGAGCATTGAGTAACCT 647
QY 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
Db 648 AATATAGAGTGATTGGAACCAAGTGTAGTGAGGCTTATGGGAGAG----- 698
QY 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 699 CTATTGGGTGGATTGAAGGTGAAGATGTTTACTGGGGAAGTTTCGGATTTCGAGTT 758
QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
Db 759 TCGGGTTGTTTTCGCCATGCGCATGACCGGCTACTAAGTTTTCGACGGCGAGTTA 818
QY 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
Db 819 GAGTTGGATTCTGATGGGTATGTTGACTAAGCCGGGAGCACCCTTGACCAGTGTAAAG 878
QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
Db 879 GTGTGTTGCTGCTGGTGAATGTGAGTAGAAGATAGTAGCAAGCTATTACAGCTGCT 938
QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGlu 322
Db 939 GGCTCAGGTGATGGCAGCTTAGATGCCGAACATTACTTCCAAGAA 986

RESULT 4
CK292570
LOCUS
DEFINITION
  ES755284 Nicotiana benthamiana mixed tissue cDNA library,
  normalized, full-length Nicotiana benthamiana cDNA clone NEMCA40 5'
  end, mRNA sequence.
ACCESSION
  CK292570.1 GI:39874140
VERSION
  EST.
KEYWORDS
  Nicotiana benthamiana
  Nicotiana benthamiana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; lamids; Solanales; Solanaceae; Nicotiana.
  1 (bases 1 to 946)
REFERENCE
  Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
  Staskawicz, B., Jin, H. and Baker, B.
  Generation of EST sequences from Nicotiana benthamiana
  Unpublished (2003)
  Other ESTs: EST755285
  Contact: Robin Buell
  The Institute for Genomic Research
  9712 Medical Center Dr, Rockville, MD 20850, USA
  Email: potato-array@tigr.org
  Clones can be requested from TIGR via potato@tigr.org

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FEATURES
  source
    Seq primer: ATT TAG GTG ACA CTA TAG.
    Location/Qualifiers
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        /mol_type="mRNA"
        /db_xref="taxon:4100"
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        /tissue_type="abiotic and biotic stress-treated leaves,
        callus tissue and root tissue"
        /lab_hosts="DH10B-Tona"
        /clone_lib="Nicotiana benthamiana mixed tissue cDNA
        library, normalized, full-length"
        /notes="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
        supplier: RNA was isolated from Nicotiana benthamiana
        tissues that include callus, roots from liquid culture
        grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
        cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
        challenged leaves (Pseudomonas syringae pv tomato 12 hr;
        Xanthomonas campestris pv campestris 12 hr, 18hr;
        Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
        campestris pv vesicatoria 18hr). RNA was isolated from
        these tissues and pooled in approximately equal molar
        amounts."
ORIGIN
  Alignment Scores:
    Pred. No.: 9,11e-136 Length: 946
    Score: 1324.50 Matches: 257
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    Best Local Similarity: 81.07% Mismatches: 30
    Query Match: 77.50% Indels: 5
    DB: 14 Gaps: 2
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  QY 10 ArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAla 29
  Db 3 AAAACCCGCCCTCTGTATCATCGCAGCGGCCGCCAGCTCATACAGCGCCATTACGCC 62
  QY 30 AlaArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAla 49
  Db 63 GCACGTCCGAGCTAAAGCCGATTTCTTTGAAGATGGATGGCTAAACGACATAGCTCCC 122
  QY 50 GlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIle 69
  Db 123 GGTGGTCAGCTTACGACCAACCCAGCTCGAAGACCTTTCCGGTTTCCCTGGAAGTATT 182
  QY 70 MetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIle 89
  Db 183 GGCGGTGGTGAGCTTATGGAACGGTGCCTGGCGAGTCTGTTCTCGGAGCTCAAAATT 242
  QY 90 LeuSerGluThrValThrAlaValAspPheSerAlaCysProPheA-gValSerAlaAsp 109
  Db 243 CATACTGAAACTGTAACCTAAAGTTGACTTTTCTAAAAGTCTCTTTGAGATTGTTTGGTCT 302
  QY 110 SerThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGlu 129
  Db 303 GATAGGACTGTGTAGCTGAAGCCGCTCATTTGTTCTACCGCTGCTGTAGCTAAGCGGCTT 362
  QY 130 HisPheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCysAlaVal 147
  Db 363 GAAATTCGGCGCTCCGCAATGACGGGTTCTCGGAATAGGGGAATTTCCGGCTTGGCCGTT 422
  QY 148 CysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyAsp 167
  Db 423 TGTACGGTGGCGCTCCGATTATTTAGGAATAGCCGTTGGCGGTGATTGGTGGGGAT 482
  QY 168 SerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIleHis 187
  Db 483 TCAGCAATGGGAAGAGCTAAATTTTGTGCTAAATATGCTTTCTAAAGTGTATATTATCAT 542
  QY 188 ArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnProLys 207
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ORIGIN

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Score: 1412.00 Matches: 273
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 82.62% Indels: 0
DB: 29 Gaps: 0

US-10-005-429-25 (1-331) x CG300268 (1-871)

QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
DB 52 ATGGAGGATCGCGCGCGCTCGCTCGCGCGCATCGCATCGCGAGCGTCC 111
QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
DB 112 GTTGCGCACACGGCAGCCATCTACGGCGCGCGCGCGAGCTCAGGCTGTGCTCTTCGAG 171
QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
DB 172 GCTGATGCGCAACGACATCGCGCGCGCGCGAGCTCACCACCGACCGCTCGAG 231
QY 61 AsnPheProGlyPheProGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
DB 232 AACTTCGCGGCTTCCCAACGACATCGCGCGCGCGAGCTCATGAGCACTGCGCGCG 291
QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
DB 292 CAGTCCCTCGCTTGGCAACACATCTCTCCGAGACCGCTCACCAGCGCTCGACTTTTCG 351
QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAlaValIleVal 120
DB 352 GCGTGCCTTCCGAGTTAGTCAGACTCCACACCGCTCCGCCGATGCGGTATCGTT 411
QY 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
DB 412 GCACCGGAGCGCTCGCGCGCGCTCCACTTCCCGCGGTCCCATGCTACTGTAACCGC 471
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
DB 472 GGCATCTCGCGCTGCTGTCAGCGTCCCGCGCGCGCGCTTCCGTAACAGCGCCATC 531
QY 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGly 180
DB 532 GCGCTCATAGCGCGCGCGACTCCGCTATGAGAGTCCCATTTCTCACCAGTACGCG 591
QY 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
DB 592 TCCACGCTCTACATCATCCACCGCGCGCAATACCTTCGTCGCTTCCAGATCATGACGCG 651
QY 201 ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyr 220
DB 652 AGGCGCTTGAGAACCCCAAAATTAGGCTCTCTCGGAGCTCGGAAGTTGTGCGAGCGCTAT 711
QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
DB 712 GCGCGCGCAACGCGCGCCCTTGGCTGGCGTAAAGGTTAAGAACCTTACTGAATGTGAG 771
QY 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
DB 772 GTCTCGGATCTCAGGTGTCTGGCTCTCTTCGCCATCGCGCATGAGCGCGGACCA 831
QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyr 273
DB 832 TTCTGCGCGGACGCTTGAATCGATTCAGATGGTTAT 870

RESULT 3
CK294886

LOCUS CK294886 988 bp mRNA linear EST 15-DEC-2003
DEFINITION EST7575600 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMCQ77 5',
end, mRNA sequence.
ACCESSION CK294886
VERSION CK294886.1 GI:39878724
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 988)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT The Institute for Genomic Research
Contact: Robin Buell
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source location/Qualifiers
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/organism="Nicotiana benthamiana"
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/db_xref="taxon:4100"
/clone="NBMCQ77"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Alignment Scores:
Pred. No.: 7,55e-136 Length: 988
Score: 1325.50 Matches: 259
Percent Similarity: 88.92% Conservative: 22
Best Local Similarity: 81.98% Mismatches: 30
Query Match: 77.56% Indels: 5
DB: 14 Gaps: 2

US-10-005-429-25 (1-331) x CK294886 (1-988)

QY 9 LeuArgThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyr 28
DB 48 CTAATAAACCCGCTCTGTATCATCGAGCGCGCGCGCTCATACGCGCGCATTTAC 107
QY 29 AlaAlaArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAla 48
DB 108 GCGCGACGTCGCGAGCTGAAGCCGATTCCTTTGAAGGATGATGCTAACGACATAGCT 167
QY 49 AlaGlyGlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGly 68
DB 168 CCGCGCGGTACGCTACGACCAACCGGATGTCGAGAACTTTCGCCGTTTCTTGAAGT 227
QY 69 IleMetGlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsn 98
DB 228 ATTGGCGGTGTGAGCTTATGACCGGTGCGCGCTGCGCTGCTTCTGTTGCGGACCAA 287

AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whiteitt, M.S.,
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Design of
 Maize Mapping Project/DuPont Consensus Sequences for Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1380)
AUTHORS Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones,
 these are publicly available from ZMDB and may be found by BLAST
 searching at MSL, maizemap.org; ZMDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZMDB:
www.zmdb.iastate.edu.

FEATURES Location/Qualifiers
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 Library"
 /note="this sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

ORIGIN

Alignment Scores:
 Pred. No.: 4,19e-178 Length: 1380
 Score: 1709.00 Matches: 331
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-10-005-429-25 (1-331) x AV104846 (1-1380)

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 DB 183 GTCTGGCACACGGACGACATCTACGGCGCCGCGGAGCTCAAGCCTGTGCTCTTCGAG 242
 QY 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrAspValGlu 60
 DB 243 GGCTGGATGGCCAAACGACATCCCGCGGGCGGGAGCTCACACCACCGACGCTCGAG 302
 QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
 DB 303 ACTTTCGGGGTTCCTCCCAACGGCATCATGGCGCGGAGCTCATGGACACTGCGCGGG 362
 QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
 DB 363 CAGTCCCTCGCTTTGGCCACCAACATCTCTCCGAGACCGCTCACCGCGCTGCACTTTTCG 422
 QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
 DB 423 GCTTGCCCATTCGAGTTAGTCACACTCCACACCGTCCTCGCGAGTGGGTATCGTT 482
 QY 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
 DB 483 GCCACGGAGCGGTCCGGCGGGCGCTCCACTTCCCGGGTCCGATCGATCTGGAACCGC 542
 QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnIleProIle 160

DB 543 GGCATCTCCGCTCTGCGCTCTGTGACGGTCCGCCGCCCATCTTTCGTAACAAGCCCATC 602
 QY 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGly 180
 DB 603 GCCGTCTATAGCGGGCGGACTCCGCTATGAGGAGTCCCAATTTCTCCCAAGTACCGC 662
 QY 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
 DB 663 TCCACAGCTCTACATCATCCACCGCGCAATACCTTCCTGCTTCCAGATCATGAGGCC 722
 QY 201 ArgAlaLeuGluAsnProLysIleGlyValLeuTrpAspSerGluValGluAlaTyr 220
 DB 723 AGGGCGCTTGAGACCCCAAAATTAAGTCTCTCTGGGACTCGGAAGTTGTTCGAGCCCTAT 782
 QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
 DB 783 GCGCGGCGCAACGGCGGCCCATTCGCTGGCGTAAGGTTAAGAACCTACTGAATGGTGAG 842
 QY 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
 DB 843 GTCTCGGATCTTCAGGTGCTCTGGGCTCTTCTTCGCCATCGGGCATGAGCGCGGACCAA 902
 QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
 DB 903 TTCTCGCGCGACAGCTTGAATCGATTCAGTGGTATGTGGAAACCAAGCCAGGTTC 962
 QY 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
 DB 963 ACTCACACCACTGTAAAGGGTGTATTTGCTCTCGCGACGTGCGAGGACAGAGTACCGT 1022
 QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
 DB 1023 CAGGCCATTACTGCCGCTGGATCAGGGTGCATGCTGCTTGGACCTGACACTACCTG 1082
 QY 321 GlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
 DB 1083 CAGGAGATCGGTGCGACAGGAGGAAAGTCTCAT 1115

RESULT 2
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 ACCESSION CG300268
 VERSION CG300268.1 GI:34214482
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 871)
 AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nurnberg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Other GSSs: OG2AE91TH
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: Tg
 Class: sheared ends
 Location/Qualifiers
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 /db_xref="taxon:4577"
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: May 5, 2004, 03:03:23 ; Search time 3070.26 Seconds
(without alignments)
3219.395 Million cell updates/sec

Title: US-10-005-429-25
Perfect score: 1709
Sequence: 1 MEGSAAPLRICITIGSGP.....AALDAHYLQETGAQEGKSD 331

Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOCALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em_esthum:*
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29: gb_gss2:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	1709	100.0	1380	11	AY104846	AY104846 Zea mays
2	1412	82.6	871	29	CG300268	CG300268 OGA2AE91TV
3	1325.5	77.6	988	14	CK294886	CK294886 EST757600
4	1324.5	77.5	946	14	CK292570	CK292570 EST755284
5	1304.5	76.3	981	14	CK283459	CK283459 EST746181
6	1267.5	74.2	976	14	CK289722	CK289722 EST752444
7	1262.5	73.9	970	14	CK278585	CK278585 EST724663
8	1255.5	73.5	947	14	CK286466	CK286466 EST749188
9	1251.5	73.2	993	14	CK250238	CK250238 EST733875
10	1239.5	72.5	946	14	CK258706	CK258706 EST742343
11	1235.5	72.3	943	14	CK252016	CK252016 EST735653
12	1222.5	71.5	930	14	CK289221	CK289221 EST751943
13	1206.5	70.6	981	14	CK270016	CK270016 EST716094
14	1202.5	70.4	920	14	CK280506	CK280506 EST743228
15	1202.5	70.4	995	14	CK255109	CK255109 EST738746
16	1200.5	70.2	933	14	CK298849	CK298849 EST761563
17	1198.5	70.1	958	14	CK245751	CK245751 EST729388
18	1198.5	70.1	962	14	CK257667	CK257667 EST741304
19	1191.5	69.7	927	14	CK296353	CK296353 EST759067
20	1191.5	69.7	937	14	CK265799	CK265799 EST711877
21	1184.5	69.3	950	14	CK255628	CK255628 EST739265
22	1183.5	69.3	934	14	CK296331	CK296331 EST759045
23	1181.5	69.1	897	14	CK246992	CK246992 EST730829
24	1176.5	68.8	910	14	CK285686	CK285686 EST748408
25	1156.5	67.7	935	14	CK254145	CK254145 EST737782
26	1151.5	67.4	968	14	CK243644	CK243644 EST727281
27	1150.5	67.3	901	14	CK296358	CK296358 EST759072
28	1144.5	67.0	908	14	CK298635	CK298635 EST761349
29	1143.5	66.9	907	14	CK280632	CK280632 EST743354
30	1136	66.5	783	14	CB673195	CB673195 OSUNE007J
31	1135	66.4	729	14	CD881998	CD881998 F1.104P10
32	1130.5	66.1	915	14	CK254872	CK254872 EST738509
33	1128.5	66.0	924	14	CK244678	CK244678 EST728315
34	1127.5	66.0	891	14	CK288120	CK288120 EST750842
35	1125.5	65.9	874	14	CK291485	CK291485 EST754199
36	1119.5	65.5	950	14	CK274289	CK274289 EST720367
37	1118.5	65.4	968	14	CK258564	CK258564 EST742201
38	1116.5	65.3	893	14	CK284817	CK284817 EST747539
39	1114.5	65.2	982	14	CK296140	CK296140 EST758854
40	1112	65.1	958	11	AY105128	AY105128 Zea mays
41	1109.5	64.9	854	14	CK291401	CK291401 EST754115
42	1104.5	64.6	929	14	CK253514	CK253514 EST737151
43	1102.5	64.5	955	14	CK290438	CK290438 EST753152
44	1098.5	64.3	841	14	CK297625	CK297625 EST760339
45	1097	64.2	861	14	CB643663	CB643663 OSUNE004H

ALIGNMENTS

RESULT 1
AY104846
LOCUS Zea mays
DEFINITION Zea mays PCC061833 mRNA sequence.
ACCESSION AY104846
VERSION AY104846.1 GI:21207924
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1380)

1380 bp mRNA linear HTC 16-OCT-2002

CC a first sequence to regulate transcription, a second DNA sequence
CC encoding a fusion polypeptide, comprising a sequence encoding an oleosin
CC gene and sequence encoding (1) and a third sequence encoding a
CC termination region functional in the host cell and growing the host cell
CC to produce a fusion polypeptide. The method or (1) is useful for
CC expression of a thiorodoxin or thiorodoxin reductase by a host cell. This
CC sequence encodes Arabidopsis thaliana thiorodoxin reductase
XX
SQ Sequence 3787 BP; 1221 A; 677 C; 621 G; 1268 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3 91e-126 Length: 3787
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservative: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 4
Gaps: 1
DB:

US-10-005-429-25 (1-331) x ABS53098 (1-3787)

QY 11 ThrArgileCysilelleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
DB 1579 ACAAGGCTCTGTATCGTAGGAGTGGCCACACGGCGGCACACACGGCGGCGATTACGCGAGCT 1638
QY 31 ArgAlaGluLeuLysProValLeuLeuPheGluGlyTyrMetAlaAsnAspIleAlaGly 50
DB 1639 AGGGCTGAACCTTAACCTCTCTCTCGAAGGATGGATGCTAACGACATCGCTCCCGGT 1698
QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
DB 1699 GGTCACCTAACCAACACCGACGCTGAGAAATTTCCCGGATTTCCAGAGGATTTCTC 1758
QY 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
DB 1759 GGAGTAGAGCTCACTGACAAATTCGGTAAACAAATCGGAGCGATTCGGTACTACGATATT 1818
QY 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
DB 1819 ACAGAGACGGTGACGAAGTGGATTCTCTCGAAGCCGTTTAAGCTATTACAGATTCA 1878
QY 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArgLeuHis 130
DB 1879 AAAGCCATTCTCGCTGACGCTGTGATTCCTGCTACTGGAGCTGTGGCTAAGCGGCTTAGC 1938
QY 131 Phe-----ProGlySerAspAlaTyrTyrAsnArgGlyIleSerAlaCysAla 146
DB 1939 TCGTTGGATCTGGTGAGGTTCTGGAGGTTCTTGGAACCGTGAAATCTCCGCTTGCT 1998
QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
DB 1999 GTTTGGACGGAGCTGCTCGATATTCGTAACAACTCTTGGGTGATCGGTGGAGGC 2058
QY 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
DB 2059 GATTACGAAATGGAAGCAAACTTCTTACAAATATGGATCTAAAGTGATATAATC 2118
QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaLeuGluAsnPro 206
DB 2119 CATAGAGAGATCTTTAGAGGCTTAAGATTATGACGAGCGAGCTTTGTCTAATCT 2178
QY 207 LysIleLysValLeuTrpAspSerGluValGluAlaTyrGlyGlyAlaAsnGlyGly 226
DB 2179 AAGATTGATGTGATTTGGAACCTGCTGTGTGTGGAAGCTTTATGGAGATGGAGAAAGAGAT 2238
QY 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
DB 2239 GTGCTTGGAGATTTGAAGTGAAGATGTGGTACCAGAGATGTTCTGATTTAAAGTT 2298
QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
DB 2299 TCTGGATTGTTCTTTGCTATTTGGTTCATGAGCCAGCTACCAAGTTTGTGGATGGTGT 2358
QY 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286

DB 2359 GAGTTAGATTGGATGGTTATGTTGTACGAGCCTGGTACTACACAGACTAGCGTTCCC 2418
QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
DB 2419 GGAGTTTTCGCTGCGGTTGATTTTCAAGATAGAAGTATAGGCAAGCCATCACTGCTGCA 2478
QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
DB 2479 GGAACCTGGGTGCATGCGAGCTTTGGATGCGAGAGCATTTACTTACAAGAGATTGGATCTCAG 2538
QY 327 GluGlyLysSerAsp 331
DB 2539 CAAGGTAAAGATGAT 2553
Search completed: May 5, 2004, 03:24:26
Job time : 437.882 secs

recombinant polypeptide (P1, P2), where P1 is capable of associating with P2 to form the MPC and associating the complex with an occlusion body (OB) through an OB-targeting-protein capable of associating with OB and P1. M1 is useful for producing an oil body associated with a recombinant MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care product which reduces the oxidative stress on the surface area of the human body or used to lighten the skin, or a pharmaceutical composition used to treat chronic obstructive pulmonary disease (COPD), cataracts, diabetes, envenomation, bronchiopulmonary disease, psoriasis, malignancies, reperfusion injury, wound healing, sepsis, gastro intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP0677 to CC ABP0964 represent sequence given in the exemplification of the present invention

SQ Sequence 3787 BP; 1221 A; 577 C; 621 G; 1268 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.91e-126 Length: 3787
 Score: 1318.00 Matches: 254
 Percent Similarity: 86.77% Conservative: 28
 Best Local Similarity: 78.15% Mismatches: 39
 Query Match: 77.12% Indels: 4
 DB: 6 Gaps: 1

US-10-005-429-25 (1-331) x ABN89582 (1-3787)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
 Db 1579 ACAGGCTCTGTATCGTAGGAGTGGCCGCGGACACACGCGGGCGATTCACGAGCT 1638
 Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
 Db 1639 AGGGCTGAACCTTCTCTCTCGAAGGATGGATGGCTAACGACATCGCTCCCGGT 1698
 Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
 Db 1699 GGTCACTTACACACACCGAGCTCGAGATTTCCCGGATTTCCAGAGGTATCTC 1758
 Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
 Db 1759 GGAGTAGAGCTCACTGACAAATTCGTAACAAATCGGACGATTCGGTACTACGATATT 1818
 Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
 Db 1819 ACAGAGCGGTGACGAAAGTGGATTTCTTCGAACCGTTTACGCTATTCCACAGATTCA 1878
 Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGlyLeuHis 130
 Db 1879 AAAGCCATTCTCGTACGCTGTGATTCTCGCTACTCGAGCTGTGGCTTAAGCGGCTTAGC 1938
 Qy 131 Phe-----ProGlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
 Db 1939 TTCTGTGGATCTGGTGAAGTCTCGAGGTTCTCGAACCCTGGAATCTCCGCTGTGCT 1998
 Qy 147 ValCysAspGlyValAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
 Db 1999 GTTTCGACGAGCTGCTCCGATATTCGTAACAACTCTTCGGTGTATCGGTGAGGAC 2058
 Qy 167 AspSerAlaMetGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
 Db 2059 GATTTCAGCAATGGAAGACCAACTTCTTACAAAATATGGATCTTAAAGTGTATATAATC 2118
 Qy 187 HisA-GATcAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
 Db 2119 CATAGAGAGATGCTTTTAGAGCGTCTAAGATTATGCGACGACGAGCTTGTCTAATCT 2178
 Qy 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyAlaAsnGlyGly 226
 Db 2179 AAGATTGATGATTGGAACTCGTCTGTTGTGAAGCTTATGGAGATGGAGAAAGAT 2238
 Qy 227 ProLeuAlaGlyValLysValLysAsnLeuGluValSerAsnGlyGluValSerAspLeuGlnVal 246

Db 2239 GTGCTGGAGGATTGAAGTGAAGAATGTGGTTACCGGAGATGTTCTGATTTAAAGATT 2298
 Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
 Db 2299 TCTGGATTGTCTTCTGATGTCTATGTCATGAGCCAGCTACCAAGTTTGGATGGTGTGTT 2358
 Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
 Db 2359 GAGTAGATTCCGATGGTATTGTTGTCACGAAGCTGGTACTACACAGACTAGCGTTCC 2418
 Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
 Db 2419 GAGTTTTCCTCGGCTGATGTCAGGATAGAGATAGGATAGGACCATCATCTGCTGCA 2478
 Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnIleGlyAlaGln 326
 Db 2479 GGAACCTGGGTGCATGGCAGCTTTGGATGCAGACATTACTTACAGAGATTGGATCTCAG 2538
 Qy 327 GluGlyLysSerAsp 331
 Db 2539 CARGTAAGAGTGTAT 2553
 RESULT 15
 ID ABS53098 standard; cDNA; 3787 BP.
 XX AC ABS53098;
 XX DT 29-NOV-2002 (first entry)
 XX DE cDNA encoding Arabidopsis thioredoxin reductase.
 XX KW Thioredoxin; thioredoxin reductase; gene expression; oleosin; oil body;
 XX KW oleosin-Chioredoxin fusion protein; Gene; ss.
 XX OS Arabidopsis thaliana.
 XX FH Key Location/Qualifiers
 XX CDS 1555..2550
 XX FT /*tag= a
 XX FT /product= "thioredoxin reductase"
 XX PN US2002088025-A1.
 XX PD 04-JUL-2002.
 XX PF 03-JUL-2001; 2001US-00897425.
 XX PR 22-FEB-1991; 91US-00659835.
 XX PR 16-NOV-1993; 93US-00142418.
 XX PR 30-DEC-1994; 94US-00366783.
 XX PR 25-APR-1997; 97US-00846021.
 XX PR 18-DEC-1998; 98US-00210843.
 XX PA (MOLO/) MOLONEY M M.
 XX PA (DALM/) DALMIA B K.
 XX PI Moloney MM, Dalmia BK;
 XX DR WPI; 2002-635723/68.
 XX DR P-FSDB; ABG32921.
 XX PT Expressing protein, by introducing chimeric nucleotide regulatory
 XX PT sequence, sequence encoding fusion protein, having sequence encoding
 XX PT protein, oleosin gene and sequence encoding termination region and
 XX PT producing protein.
 XX PS Example 21; Fig 15; 69pp; English.
 XX CC The invention describes a method of expressing thioredoxin or thioredoxin
 XX CC reductase (I) in the oil body of a host cell using an oil body protein
 XX CC gene. The method involves introducing a chimeric nucleic acid comprising

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PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161361P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 1.15e-126 Length: 1539
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservative: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 4
DB: 3 Gaps: 1

US-10-005-429-25 (1-331) x AAC36511 (1-1539)

QY 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyAlaAla 30
Db 236 ACAAGGCTCTGTATCGTAGAGTGGCCCGGCGCACACACGCGCGGATTTACGCGAGCT 295
QY 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaAlaGly 50
Db 296 AGGGCTGAACCTTAACCTCTCTCTCGAAGGATGGATGCTAACGACATCGCTCCCGGT 355
QY 52 GlyGlnIleuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 356 GGTCAACTAACACACCCACCGACGTCGAGATTTCCCGGATTTCCAGAGGTATTCTC 415
QY 71 GlyAlaAspLeuMetAspAenCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 416 GGAAGTAGAGCTCACTGACAAATTCGGTAACATCGGAGCGATTCGTACTACGATATT 475
QY 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 476 ACAGACACGGTGACGAAGTCGATTTCTCTCTCGAAACCCGTTTAAGCTATTTCACAGATTC 535
QY 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyValAlaAlaArgArgLeuHis 130
Db 536 AAAGCCATCTCGCTGACGCTGTGATTCCTGCTACTGAGCTGTGGCTTAAGCGGCTTAGC 595
QY 131 Phe-----ProGlySerAspAlaTyTrpAsnArgGlyIleSerAlaCysAla 146
Db 596 TTGGTTGGATCTGGTGAAGGTTCTGGAGGTTCTGGAAACCGTGGAAATCTCGGCTTGTGCT 655
QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGly 166
Db 656 GTTTGGACGAGCTGCTCGATATTCCGTACAAACCTCTTCGGGTGATCGGTGAGGC 715
QY 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyThrGlySerHisValTyIleIle 186
Db 716 GATTACGAATGGAAGAAGCAAACTTCTTACAAATATGGAATCTAAAGTGATATAATC 775
QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
Db 776 CATAGAGAGATGCTTTTAGGCTCTAAGATTATCGACGAGCTTTGCTTAATCT 835
QY 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyGlyAlaAsnGlyGly 226
Db 836 AAGATTGATGATTGGAACTCGTCTGTTGGAGCTTATGGAGATCGAAGAGAT 895
QY 227 ProLeuAlaGlyValLysAlaLeuAsnGlyGluValSerAspLeuGlnVal 246
Db 227 ProLeuAlaGlyValLysAlaLeuAsnGlyGluValSerAspLeuGlnVal 246

896 GTGCTTGGAGGATTGAAAGTGGAAGATGTGGTTACCGGAGATGTTTCTGATTTAAAGTT 955
247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
956 TCTGGATTGTTCTTGTCTATTGCTCATGAGCCAGCTACCAAGTTTGTGGATGGTGTGTT 1015
267 GluLeuAspSerAspGlyTyValGluThrLysProGlySerThrHisThrSerValLys 286
1016 GAGTTAGATTGGATGGTATTGTTGTCGAAAGCCCTGGTACTACAGACTACGCTTCCC 1075
287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyArgGlnAlaIleThrAlaAla 306
1076 GGAGTTTCTGCTCGCGGTGATGTTTCAGGATAGAGATAGGCAAGCATCTGCTGCA 1135
307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyLeuGlnGluLeuGlyAlaGln 326
1136 GGAACCTGGGTGATGCGCAGCTTTGGATGCGAGCATTTACTTACAGAGATTGGATCTCAG 1195
327 GluGlyLysSerAsp 331
1196 CAGGTAAAGATGAT 1210

RESULT 14
ABN89582
ID ABN89582 standard; DNA; 3787 BP.
XX
AC ABN89582;
XX
DT 06-SEP-2002 (first entry)
XX
DE Phaseolin promoter-thioredoxin reductase-phaseolin terminator DNA #22.
XX
KW Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
KW oil body; ophthalmological; antidiabetic; cytotatic; antipsoriatic;
KW vasotropic; vulnary; antibacterial; immunosuppressive; antitumor;
KW food product; milk; wheat; oxidative stress; cataract; diabetes;
KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
KW gastro oesophageal reflux disease; gene; ds.
XX
OS Arabidopsis sp.
OS Phaseolus vulgaris.
XX
PN X0200250289-A1.
XX
PD 27-JUN-2002.
XX
PF 19-DEC-2001; 2001WO-US050240.
XX
PR 19-DEC-2000; 2000US-00742900.
PR 05-JUL-2001; 2001US-0302885P.
PR 04-DEC-2001; 2001US-00006038.
XX
PA (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Van Rooijen G, Deckers H, Heifetz PS, Briggs SP, Dalmia BK;
PI Del Val G, Zaplachinski S, Moloney M;
XX
DR WPI: 2002-508806/54.
DR P-PSDB; ABP60685.
XX
PT Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.
XX
PS Example 2; Page 173-175; 362pp; English.
XX
CC The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second

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05-MAY-1999;	99US-013248456P
06-MAY-1999;	99US-01324846P
07-MAY-1999;	99US-01324847P
08-MAY-1999;	99US-01324848P
09-MAY-1999;	99US-01324849P
10-MAY-1999;	99US-01324850P
11-MAY-1999;	99US-01324851P
12-MAY-1999;	99US-01324852P
13-MAY-1999;	99US-01324853P
14-MAY-1999;	99US-01324854P
15-MAY-1999;	99US-01324855P
16-MAY-1999;	99US-01324856P
17-MAY-1999;	99US-01324857P
18-MAY-1999;	99US-01324858P
19-MAY-1999;	99US-01324859P
20-MAY-1999;	99US-01324860P
21-MAY-1999;	99US-01324861P
22-MAY-1999;	99US-01324862P
23-MAY-1999;	99US-01324863P
24-MAY-1999;	99US-01324864P
25-MAY-1999;	99US-01324865P
26-MAY-1999;	99US-01324866P
27-MAY-1999;	99US-01324867P
28-MAY-1999;	99US-01324868P
29-MAY-1999;	99US-01324869P
30-MAY-1999;	99US-01324870P
31-MAY-1999;	99US-01324871P
01-JUN-1999;	99US-01324872P
02-JUN-1999;	99US-01324873P
03-JUN-1999;	99US-01324874P
04-JUN-1999;	99US-01324875P
05-JUN-1999;	99US-01324876P
06-JUN-1999;	99US-01324877P
07-JUN-1999;	99US-01324878P
08-JUN-1999;	99US-01324879P
09-JUN-1999;	99US-01324880P
10-JUN-1999;	99US-01324881P
11-JUN-1999;	99US-01324882P
12-JUN-1999;	99US-01324883P
13-JUN-1999;	99US-01324884P
14-JUN-1999;	99US-01324885P
15-JUN-1999;	99US-01324886P
16-JUN-1999;	99US-01324887P
17-JUN-1999;	99US-01324888P
18-JUN-1999;	99US-01324889P
19-JUN-1999;	99US-01324890P
20-JUN-1999;	99US-01324891P
21-JUN-1999;	99US-01324892P
22-JUN-1999;	99US-01324893P
23-JUN-1999;	99US-01324894P
24-JUN-1999;	99US-01324895P
25-JUN-1999;	99US-01324896P
26-JUN-1999;	99US-01324897P
27-JUN-1999;	99US-01324898P
28-JUN-1999;	99US-01324899P
29-JUN-1999;	99US-01324900P
30-JUN-1999;	99US-01324901P
01-JUL-1999;	99US-01324902P
02-JUL-1999;	99US-01324903P
03-JUL-1999;	99US-01324904P
04-JUL-1999;	99US-01324905P
05-JUL-1999;	99US-01324906P
06-JUL-1999;	99US-01324907P
07-JUL-1999;	99US-01324908P
08-JUL-1999;	99US-01324909P
09-JUL-1999;	99US-01324910P
10-JUL-1999;	99US-01324911P
11-JUL-1999;	99US-01324912P
12-JUL-1999;	99US-01324913P
13-JUL-1999;	99US-01324914P
14-JUL-1999;	99US-01324915P
15-JUL-1999;	99US-01324916P
16-JUL-1999;	99US-01324917P
17-JUL-1999;	99US-01324918P
18-JUL-1999;	99US-01324919P
19-JUL-1999;	99US-01324920P
20-JUL-1999;	99US-01324921P
21-JUL-1999;	99US-01324922P
22-JUL-1999;	99US-01324923P
23-JUL-1999;	99US-01324924P
24-JUL-1999;	99US-01324925P
25-JUL-1999;	99US-01324926P
26-JUL-1999;	99US-01324927P
27-JUL-1999;	99US-01324928P
28-JUL-1999;	99US-01324929P
29-JUL-1999;	99US-01324930P
30-JUL-1999;	99US-01324931P
31-JUL-1999;	99US-01324932P
01-AUG-1999;	99US-01324933P
02-AUG-1999;	99US-01324934P
03-AUG-1999;	99US-01324935P
04-AUG-1999;	99US-01324936P
05-AUG-1999;	99US-01324937P
06-AUG-1999;	99US-01324938P
07-AUG-1999;	99US-01324939P
08-AUG-1999;	99US-01324940P
09-AUG-1999;	99US-01324941P
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11-AUG-1999;	99US-01324943P
12-AUG-1999;	99US-01324944P
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17-AUG-1999;	99US-01324949P
18-AUG-1999;	99US-01324950P
19-AUG-1999;	99US-01324951P
20-AUG-1999;	99US-01324952P
21-AUG-1999;	99US-01324953P
22-AUG-1999;	99US-01324954P
23-AUG-1999;	9

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PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
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PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 1,05e-126 Length: 1438
Score: 1318.00 Matches: 254
Percent Similarity: 86.77% Conservative: 28
Best Local Similarity: 78.15% Mismatches: 39
Query Match: 77.12% Indels: 4
DB: 3 Gaps: 1

US-10-005-429-25 (1-331) x AAC38830 (1-1438)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
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Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAenAspIleAlaAlaGly 50
Db 195 AGGCTGAACCTTAAACCTTCTCTCGAAGAGTGTGGTACGACATCGCTCCCGGT 254

Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 255 GGTCACTAACACACACACCGAGCTCGAATTTCCCGGATTTCCAGAGGTATTCCTC 314

Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 315 GGAGTAGAGCTCACTGACAAATTCGGTAAACATCGGAGCGATTCGGTACTACGATATT 374

Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 375 ACAGAGCGGTGACGAAGTCGATTTCTCTGAAACCGTTTAAGCTTATTCACAGATTCA 434

Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArgLeuHis 130
Db 435 AAGCCATCTCGCTGACGTGTGATTCCTCGTACTGAGAGCTGTGGCTTAGCGGCTTAGC 494

Qy 131 Phe-----ProGlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
Db 495 TTCGTTGGATCTGGTGAAGGTTCTGGAGGTTCTTGGAAACCGTGAATCTCCGCTTGCT 554

Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGlyGly 166
Db 555 GTTTCGACGAGCTGCTCGATATTCGTAACAAACCTCTTTCGGGTGATCGGTGAGGC 614

Qy 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
Db 615 GATTTCAGCAATGGAAGAACAACTTTCTTACAAATATGATCTAAAGTGATATAATC 674

187 HisArgArgAsnThrPheArgAlaSerLysIleIleGlnAlaArgAlaLeuGluAsnPro 206
675 CATAGGAGAGATGCTTTAGAGCGTCTAAGATTATGACGAGCGAGCTTTGTCTAATCT 734

207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
735 AAGATTGATGATTTGGAACTCTGCTGTTGTGGAAGCTTATGAGATGGAGAAAGAGAT 794

227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
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247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGlnLeu 266
855 TCTGGATTGTCTTGTCTATTTGCTATGAGCCAGTACCAAGTTTTCGATGTTGGTGTGTT 914

267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
915 GAGTTAGATTCGATGTTGTTGTCAGAACCTGTTACTACACAGACTAGGTTCC 974

287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
975 GAGATTTTCGCTGGGCTGATGTTTACAGATAGAGATATAGGCAAGCCATCCTGCTGCA 1034

307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
1035 GGAACCTGGGTCATGGCAGCTTTGGATGACAGACATTACTTCAAGAGATTGGATCTCAG 1094

327 GluGlyLysSerAsp 331
1095 CAAGGTAAGATGAT 1109

RESULT 13
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ID AAC36511 standard; DNA; 1539 BP.
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DX 17-OCT-2000 (first entry)
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DE Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX EF1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000BP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-01233548P.
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PR 25-MAR-1999; 99US-0126264P.
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PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.

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PR	02-JUL-1999;	99US-0142055P.	PR	23-SEP-1999;	99US-0155486P.
PR	06-JUL-1999;	99US-0142390P.	PR	24-SEP-1999;	99US-0155659P.
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PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.

OS Arabidopsis sp.
 XX
 PN W0200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 XX 19-DEC-2001; 2001WO-US050240.
 XX
 XX 19-DEC-2000; 2000US-00742900.
 PR
 PR 05-JUL-2001; 2001US-0302885P.
 PR
 PR 04-DEC-2001; 2001US-00006038.
 XX
 XX (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 PI MPI; 2002-508806/54.
 DR
 XX
 XX Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 XX Claim 68; Page 161-162; 362pp; English.
 PS
 XX
 XX The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, emphysema, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 XX Sequence 1002 BP; 259 A; 196 C; 272 G; 275 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 6.39e-127 Length: 1002
 Score: 1318.00 Matches: 254
 Percent Similarity: 86.77% Conservative: 28
 Best Local Similarity: 78.15% Mismatches: 39
 Query Match: 77.12% Indels: 4
 DB: 6 Gaps: 1

US-10-005-429-25 (1-331) x ABN89578 (1-1002)

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 QY 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
 DB 145 GGTCACTAAACACACCGCGCGTCAAGATTTCCCGGATTTCCAGAGGTATTTCTC 204
 QY 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
 DB 205 GGAGTAGAGTCACTGACAAATCCGTAAACATCGGAGGATTCGTACTACGATATT 264

QY 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
 DB 265 ACAGAGACGGTACGAAAGTCGATTTCTCTCGAAACCGTTTAAGCTATTTCACAGATTCA 324
 QY 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgGluHis 130
 DB 325 AAAGCCATTCTCGCTGACCTGTGATTCGCTACTTGGAGCTGTGGCTAAGCGGCTTAGC 384
 QY 131 Phe-----ProGlySerAspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
 DB 385 TTGCTTGGATCTGGTGAAGCTTCTGGAACCGTGAATCTCCGCTTGTGCT 444
 QY 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
 DB 445 GTTTCGACGGAGCTGCTCCGATATTCGTAACAAACCTCTTCGCGTGTATCGGTGGAGC 504
 QY 167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
 DB 505 GATTCAGCANTGAGAGACAAACTTCTTACAAATATGATGATCTAAAGTGTATATATC 564
 QY 187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
 DB 565 CATAGGAGAGATGCTTTTAGAGCGTCTAAGATTATGCAGACGAGCTTTGTCTAATCCT 624
 QY 207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyrGlyAlaAsnGlyGly 226
 DB 625 AAGATTGATGTGATTTGGAACTCGTCTGTGTGGAGCTTATGGAGATCGAGAAAGAGAT 684
 QY 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
 DB 685 GTCCTTGGAGGATTAAGTGAAGATGTGTTACCGGAGATGTTTCTGATTTAAAGTT 744
 QY 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
 DB 745 TCTGGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 804
 QY 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
 DB 805 GAGTTAGATTCGATGTTATGTTGTCAGAGAGCTGTTACTACACAGACTAGCGTTCC 864
 QY 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
 DB 865 CGAGTTTCTCGCTCGCGTGTGTTTTCAGGATAAGATATAGGCAAGCCATCCTGCTGCA 924
 QY 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
 DB 925 GGAACTGGGTGATGCGACGCTTTGGATGCGAGCATTACTTACAGAGATTGGATCTCAG 984

QY 327 GluGlyLysSerAsp 331
 DB 985 CAAGGTAAGAGTGTAT 999

RESULT 10
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 ID ABN89576 standard; DNA; 1002 BP.
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 AC ABN89576;
 XX
 DT 06-SEP-2002 (first entry)
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 DE Arabidopsis NADPH thioredoxin reductase DNA SEQ ID NO:8.

XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 XX oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
 XX vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 XX food product; milk; wheat; oxidative stress; cataract; diabetes;
 XX chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
 XX bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 XX gastro intestinal bleeding; intestinal bowel disease; ulcer;
 XX gastro oesophageal reflux disease; gene; ds.
 XX Arabidopsis sp.
 OS

[illegible]

Db 979 GTGACCAAGCCAGGCTACTTAAGACGAGCGTGGTGGTATTTGCTGCTGGAGATGTT 1038
 Qy 295 GlnAspLysLysTyrArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu 314
 Db 1039 CAAGACAAGAGTATAGACAGCCCATCTGCTGAGGAAGTGGGTGATGGCGCATTTG 1098
 Qy 315 AspAlaGluHisTyrLeuGlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
 Db 1099 GATCGACAGCATTAATTACAGAGATGGATCTCAGGAGGGTAAAGATGAT 1149

RESULT 7
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 ID ADA67905 standard; DNA; 1152 BP.
 AC ADA67905;
 XX 20-NOV-2003 (first entry)
 DE Arabidopsis thaliana gene, SEQ ID 148.
 XX Plant; bacterial infection; fungal infection; viral infection; ds.
 KW Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 PN WO200300898-A1.
 XX 03-JAN-2003.
 XX 22-JUN-2001; 2001WO-IB0011105.
 XX 22-JUN-2001; 2001WO-IB001105.
 PR (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI, 2003-175290/17.

PT Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX Claim 6; SEQ ID NO 148; 899pp; English.
 CC The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 SQ Sequence 1152 BP; 281 A; 222 C; 308 G; 341 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,18e-128 Length: 1152
 Score: 1335.50 Matches: 258
 Percent Similarity: 86.65% Conservative: 34
 Best Local Similarity: 76.56% Mismatches: 36
 Query Match: 78.15% Indels: 9
 DB: 7 Gaps: 2

US-10-005-429-25 (1-331) x ADA67905 (1-1152)
 Qy 4 SerAlaAlaAlaProLeu-----ArgThrArgLeCysIleLeGlySer 18
 Db 139 TCGCGCGCGCGCGCGTGCACATGGAACATCAACAAACCAAGGTTGCTGCGGAGT 198

Qy 19 GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38
 Db 199 GGACCAAGCAGCACACACGCGCGGATCTATGCATCGAGACGCGGCTTAAGCCCTCTTC 258
 Qy 39 PheGluGlyTyrMetAlaAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrAsp 58
 Db 259 TTGAGAGATGGATGGCTAACGACATGCTCCCGCGGTCAATTAACACAAACCGAC 318
 Qy 59 ValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCys 78
 Db 319 GTCGAAAACCTCCCTGGGTTCCTGAGGTATTCCTCGTATTGATATCGTTGGAATTC 378
 Qy 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAsp 98
 Db 379 AGAAAAACAATCGGAGAGATTTGGACATACCATCTTCACGGAACCTGTTAACAAAGTTGAT 438
 Qy 99 PheSerAlaCysPropheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
 Db 439 TTCTCATCGAAACCGTTTAAAGCTATTCACGTATTCGAGAACTGTTCCTCGTATCTGTA 498
 Qy 119 IleValAlaThrGlyAlaValAlaValIleGlyCysAspSerAlaMetGluGluSerAsn 134
 Db 499 ATCAATTTCTCTGAGCTGTGCTAAACGCTTAGCTTCTAGCTTCTGATCTGGTGAAGTTAAT 558
 Qy 135 AspAlaTyrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
 Db 559 GGTGTTTTTGGAAATCGTGGTATCTCCGCTTGTCTGTTGCGACGAGCTGCTCCGATT 618
 Qy 155 PheArgAsnLysProIleAlaValIleGlyCysAspSerAlaMetGluGluSerAsn 174
 Db 619 TTTAGGAATAAGCCTCTTGTGTTATTTGGTGGTGGTATTCAGCTATGGAGGAAGCGAAT 678
 Qy 175 PheLeuThrLysTyrGlySerHisValTyrIleIleHisArgArgAsnThrPheArgAla 194
 Db 679 TTTCTGCTAAGTATGATGATTAAGTTTATATTATTATTCATAGGAGGATACGTTTAGGCG 738
 Qy 195 SerLysIleMetGlnAlaArgAlaLeuGluAsnProLysIleLysValLeuThrAspSer 214
 Db 739 TCTAAGATTATGACAGCAGAGAGCTTTGCTTAACCTTAAGATTGAAGTGATTTGAAGCTCT 798
 Qy 215 GluValValGluAlaTyrGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLys 234
 Db 799 GCGTGGTTGAGCGTATGCTGATGAAATGGAGCTGCTCTTGGAGGATTCAGAGTGAAG 858
 Qy 235 AsnLeuLeuAsnGlyGluValSerAspLeuGlnValSerGlyLeuPheAlaIleGly 254
 Db 859 AATGTTGTTACTCGGATGTTTCAGATCTGAAGGTGCTCGATTTGCTTTGCTATTGCT 918
 Qy 255 HisGluProAlaThrLysPheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrVal 274
 Db 919 CATGAGCCAGCTACGAAGTTTTTGGATGGCGAGCTTGAAGCTTGAATGAGATGTTATGTT 978
 Qy 275 GluThrLysProGlySerThrHisThrSerValLysGlyValPheAlaAlaGlyAspVal 294
 Db 979 GTGACCAAGCCAGGCTACTTACTTAAGACGAGCGTGGTGGTATTTGCTGCTGAGATGTT 1038
 Qy 295 GlnAspLysLysTyrArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu 314
 Db 1039 CAAGACAAGAGTATAGACAGCCCATCTCCTCGAGGAAGTGGGTGATGGCGCATTTG 1098
 Qy 315 AspAlaGluHisTyrLeuGlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
 Db 1099 GATCGACAGCATTAATTACAGAGATTTGATCTCAGGAGGGTAAAGATGAT 1149

RESULT 8
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 ID AAC48213 standard; DNA; 1375 BP.
 XX AAC48213;
 AC AAC48213;
 DT 18-OCT-2000 (first entry)
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QY 195 SerLysIleMetGlnAlaArgAlaLeuGluAenProLysValLeuThrPaspSer 214
 DB 739 TCTAAGATTATGAGCAGAGAGCTTTGTTAAACCTTAAGATTGAAGTATTGGAACTCT 798
 QY 215 GluValValGluAlaThrGlyGlyAlaAenGlyGlyProLeuAlaGlyValLysValLys 234
 DB 799 GCCGTGTTGAGCGGATGATGATGATAAATGACGGTCTTCTGGAGGATTGAAGGTGAAG 858
 QY 235 AsnLeuLeuAenGlyGluValSerAspLeuGlnValSerGlyLeuPheAlaIleGly 254
 DB 859 AATGTTGTTACTGGGGATGTTTCTAGATCTGAAGGTCTCTGGATGTTCTTTGCTATTGTT 918
 QY 255 HisGluProAlaThrLysPheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrVal 274
 DB 919 CATGACCGAGCTACGAAGTTTGTGATGGCGACCTTGACCTTGATGAAGTGTATTGTT 978
 QY 275 GluThrLysProGlySerThrHisThrSerValLysGlyValPheAlaAlaGlyAspVal 294
 DB 979 GTGACCAAGCAGGTACTTAAGACGAGCGGTGTTGTTGGTGTATTCTGCTGAGATGTT 1038
 QY 295 GlnAspLysIleThrArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu 314
 DB 1039 CAAGCAAGAGATATAGACAGGCACTCATCTGTCAGAGACTGGGTGCTGGCGGATG 1098
 QY 315 AspAlaGluHisThrLeuGlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
 DB 1099 GATGCAGAGCATTACTTACAAGAGATTGGATCTCAGAGCGGTAAAGATGAT 1149

RESULT 6
 ABZ14681
 ID ABZ14681 standard; DNA; 1152 BP.

XX ABZ14681;
 DT 21-JAN-2003 (first entry)
 XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2486.
 XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX Arabidopsis thaliana.
 XX Arabidopsis thaliana.
 XX W0200216655-A2.
 XX 28-FEB-2002.
 XX 24-AUG-2001; 2001WO-US026685.
 XX 24-AUG-2000; 2000US-0227866P.
 XX 26-JAN-2001; 2001US-0264647P.
 XX 22-JUN-2001; 2001US-0300111P.
 XX (SCRI) SCRIPPS RES INST.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Harper JF, Kreps J, Wang X, Zhu T;
 XX WPI; 2002-304127/34.

Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
 Claim 144; SEQ ID NO 2486; 577pp + Sequence Listing; English.
 The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used

CC in methods of the invention. Note: The sequence data for this patent is CC not represented in the printed specification but is based on sequence CC information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 1152 BP; 281 A; 222 C; 308 G; 341 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,18e-128 Length: 1152
 Score: 1335.50 Matches: 258
 Percent Similarity: 86.65% Conservative: 34
 Best Local Similarity: 76.56% Mismatches: 36
 Query Match: 78.15% Indels: 9
 DB: 6 Gaps: 2
 US-10-005-429-25 (1-331) x ABZ14681 (1-1152)

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 DB 139 TCCGCGCGCGCGCGCGTGCACATGGAAACTCAAAACCAAGGTTTGCATGTCGGAAGT 198
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 QY 59 ValGluAenPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCys 78
 DB 319 GTGCAAACTTCCCTGGGTCCCTGAGGATTTCTCGGTATTGATATGTTGAGAAATTC 378
 QY 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAsp 98
 DB 379 AGAAAAACAATCGAGAGATTTGGAACACGATCTTCAACGAAACTGTTAAACAAAGTTGAT 438
 QY 99 PheSerAlaCysProPheArgValSerAlaAspSerThrValLeuAlaAspAlaVal 118
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 QY 119 IleValAlaThrGlyAlaValAlaArgArgLeuHisPheProGlySer----- 134
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 DB 559 GGTGTTTGTGAATCGTGTATCTCCGCTTGTGCTGTTGTCGACGAGCTCTCGGAT 618
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 QY 255 HisGluProAlaThrLysPheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrVal 274
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 QY 275 GluThrLysProGlySerThrHisThrSerValLysGlyValPheAlaAlaGlyAspVal 294

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PR 28-OCT-1999; 99US-0161932P.
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PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 1,18e-128
Score: 1335.50
Percent Similarity: 86.65%
Best Local Similarity: 76.56%
Query Match: 78.15%
DB: 3

US-10-005-429-25 (1-331) x AAC43307 (1-1152)

QY 4 SerAlaAlaProLeu-----ArgThrArgIleCysIleIleGlySer 18
DB 139 TCCGCCGCCGCCGCCGCCGACATGCAACCAACCAAGTTTCATCGTCGGAAT 198
QY 19 GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38
DB 199 GGACCAGCAGCACACACGGCGGGGATCTATGATCGTAGAGCGGAGCTTAAGCCTCTTC 258
QY 39 PheGluGlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAsp 58
DB 259 TTCGAGGATGGATGGCTAACGACATCGCTCCCGGGGTCAATTAACCTACCAACCGAC 318
QY 59 ValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCys 78
DB 319 GTCGAAACCTCCCTGGGTTCCCTGAAGGTATTCGGTATTCATATCGTTGAGAAATTC 378
QY 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAsp 98
DB 379 AGAAACAATCGGAGAGATTGGAACTACGATCTTCACGGAACCTGTTAACAAAGTTGAT 438
QY 99 PheSerAlaCysPropheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
DB 439 TTCTCATCGAAACCGTTTAAGTATTACTGATTCGAGAACTGTTCTGCTGATTCGTGA 498
QY 119 IleValAlaThrGlyAlaValAlaAlaArgLeuHisPheProGlySer----- 134
DB 499 ATCAATTCATCGAGCTGTTGTAAACGCTTAGCTTACTGATCTGGTGAAGTAAT 558
QY 135 AspAlaTyrTrpAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
DB 559 GGTGGTTTTTGAATCGTGATACTCCGCTTGCTGTTTGGCGAGCGAGCTGCTCGGAT 618
QY 155 PheArgHisLysProIleAlaValIleGlyGlyAspSerAlaMetGluGluSerAsn 174
DB 619 TTAGGAATAGCCCTCTGTGGTATTGGTGGTGGTATTCAGCTATGAGGAGGAGGAAT 678
QY 175 PheLeuThrLysTyrGlySerHisValTyrIleIleHisArgArgAsnThrPheArgAla 194
DB 679 TTCTGACTAAGTATGATCTAAGGTTTATATTATTATTCATAGGAGGATACGTTTAGGGCG 738

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Db 361 GCACCGCGCGCTCGCCGGGAGCTCCACTTCGCGGCTCGAGCGCTTACTGGAACCGC 420
QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 421 GGCATTCGCGCTCGCGCGCTGCGCGGGGGCGCCCAATTTTCAGGACAAACCCATC 480
QY 161 AlaValIleGlyGlyAspSerAlaMetGluSerAsnPheLeuThrLysTyrGly 180
Db 481 GCGTCATCGCGCGCGGAGCTCCGCTCGAGGAGTCCAACTTCCTCACCAGTACGCGC 540
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QY 201 ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyr 220
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Db 700 -----GGTTCGGTCTCTTCTTCGCCATCGACATGACCGGCGACGAG 744
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QY 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
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ID AAC43307 standard; DNA; 1152 BP.
XX AAC43307;
AC AAC43307;
XX 17-OCT-2000 (first entry)
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XX Arabidopsis thaliana.
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
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 DB 532 GGCATCTCGCGCTGCGCGGTCTGCGACGGCGCGCGCCCATCTTCCGGAACAGGCCCAT 591
 QY 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrIleYsTrpGly 180
 DB 592 GCCGTGCGCGGGGCGGACTCCGCCCATGGAGGAGGCCAACTCTCCCAAGTAACGCGC 651
 QY 181 SerHisValTyrIleIleHisArgAsnThrPheArgAlaSerIleIleMetGlnAla 200
 DB 652 TCCCGCGCTACATCATCATCCACCGCGCAACGCGCTTCCGCGGTCCAGATCATGCGCGC 711
 QY 201 ArgAlaLeuGluAsnProIleValLeuTrpAspSerGluValValGluAlaTyr 220
 DB 712 CGGGGCTCTCCAAACCCCAAGATCCAGTCTGCTGGGACTCCGAGGTCTGCGAGCGTAC 771
 QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValIleValAsnLeuLeuAsnGlyGlu 240
 DB 772 GCGCGCGCGCGCGGTCTGCTGGCGCGGTCAAGGTCAAGACGTGTGTGAGCGCGCGAG 831
 QY 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrIleVal 260
 DB 832 GTCTCCGACTCCAGTCCCGGGCTCTTCTCGCCATTGGACACGACCGCGCGCAAG 891
 QY 261 PheLeuGlyGlyGlnLeuLeuAspSerAspGlyTyrValGluThrIleYsProGlySer 280
 DB 892 TTTCTCGCGCGCGAGCTCGAGCTGGACTCCGATGGCTATGTGTGACCAAGCCCGGCTCC 951
 QY 281 ThrHisThrSerValIleGlyValPheAlaAlaGlyAspValGlnAspIleYsTrpArg 300
 DB 952 ACTCACACAGCGTCAAGGGAGTCTTCGCGCGCGGTGATGTTTCAGACAAAGATATCC 1011
 QY 301 GlnAlaIleThrAlaAlaGlySer 308
 DB 1012 CAGGCCATTACTCCCGCGCGATCA 1035
 RESULT 4
 ID ADA70332 standard; DNA; 963 BP.
 XX
 AC ADA70332;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Rice gene, SEQ ID 3655.
 XX
 KW plant; bacterial infection; fungal infection; viral infection; rice;
 gene; ds.

XX Oryza sativa.
 XX WO2003000898-A1.
 XX 03-JAN-2003.
 XX 22-JUN-2001; 2001WO-IB001105.
 XX 22-JUN-2001; 2001WO-IB001105.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 DR WPI; 2003-175290/17.
 XX Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX Claim 6; SEQ ID NO 3655; 899pp; English.
 XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 XX Sequence 963 BP; 159 A; 334 C; 292 G; 178 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 8,09e-132 Length: 963
 Score: 1365.00 Matches: 269
 Percent Similarity: 89.24% Conservative: 13
 Best Local Similarity: 85.13% Mismatches: 16
 Query Match: 79.87% Indels: 18
 DB: 7 Gaps: 3
 US-10-005-429-25 (1-331) x ADA70332 (1-963)
 QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
 DB 1 ATGAGGGATCCCGGGGCGCCGCTCCGACGCGGTGTGATCATCGGAGCGGGCGCG 60
 QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLeuProValLeuPheGlu 40
 DB 61 TCGGCGCACCGCGCGGATCTACCGCGCGCGCGGAGCTCAAGCCGCTCTCTCGAG 120
 QY 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlnLeuThrThrThrAspValGlu 60
 DB 121 GGTCTCTCGCCCAACGACATCGCGGGGGGGAGCTCACACCACCAACGAGCTCGAG 180
 QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
 DB 181 AACTTCCCGGGCTTCCCGACGGCATCTTCGGCGCGGACCTCATGATCGGTGCGCGCC 240
 QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
 DB 241 CAGTCCCTTCGGGTTCGGGACCAAGGATCTCTCCGAGACCGTCCACCGCGGTGCGACTCTCC 300
 QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
 DB 301 GCCCGCCCTTCCGGTCTCGGTCTCGACTCCACCGCGGTCTCGCGCGAGCGCGTCTCGTCTC 360
 QY 121 AlaThrGlyAlaValAlaArgGluLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140

CC reductase eliminates the need to develop exogenous sources for addition
CC during processing. Secondly, physical disruption of seed integrity is not
CC necessary to bring the enzyme in contact with the storage or matrix
CC proteins of the seed prior to processing or as an extra processing step.
CC The present sequence is rice NADPH dependent thioredoxin reductase DNA
CC (NTR)

XX Sequence 1560 BP; 302 A; 435 C; 439 G; 372 T; 0 U; 12 Other;

Alignment Scores:
Pred. No.: 2,97e-143 Length: 1560
Score: 1478.00 Matches: 282
Percent Similarity: 96.12% Conservative: 15
Best Local Similarity: 91.26% Mismatches: 12
Query Match: 86.48% Indels: 0
DB: 6 Gaps: 0

US-10-005-429-25 (1-331) x AAD29838 (1-1560)

Qy 1 MetGluGlySerAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
Db 406 ATGAGGAGATCCGCGGGGCGCGCTCGACGCGCTGTCATCATCGGAGCGGCGG 465
Qy 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
Db 466 TCGGCGCACACGGCGCGATCTACGCGCGCGCGCGGAGCTCAAGCGCGTCTTCGAG 525
Qy 41 GlyTrpMetAlaAsnAlaAlaGlyGlyGlnLeuThrThrThrThrThrThrThrThr 60
Db 526 GGTCTGGCTCCACACGACATCGCGCGGGGCGCGCTCACCCACACCGAGCTCGAG 585
Qy 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
Db 586 AACTTCGCGGGTTCGCGAGGCGATCTCGCGCGCGAGCTCATGTGCTGCGCGGCC 645
Qy 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGlyThrValThrAlaValAspPheSer 100
Db 646 CAGTCTCTCGGTTCGCGACGACGATCTCCGAGACCGCTCACCGCGGTTCGCTTCC 705
Qy 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db 706 GCGCGCGCTTCGCGTTCGCTCGAGTCCACACCGCTGCTCGCGCGCGCTGCTGTC 765
Qy 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
Db 766 GCCACCGCGCGCTCGCGCGGCTCACCTTCGCGCGCTCCGAGCGCTACTGGAACCGC 825
Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 826 GGCATCTCAGCTTCGCGCTTCGCGAGCGGCGCGCGCGCTTCAGAGACCAACCCATC 885
Qy 161 AlaValIleGlyGlyAspSerAlaMetGluLysSerAsnPheLeuThrLysTyrGly 180
Db 886 GCGCTCATCGCGCGCGACTCCGCCATGAGGAGTCCAACTTCCTCCCAAGTACGGC 945
Qy 181 SerHisValTrpIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 946 TCCCATGTGTACATATCCACCGCGCGACACCTTCGCGCGCTCCAGATCATCGAGGCC 1005
Qy 201 ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValGluAlaTyr 220
Db 1006 AGGCGGTGTCAAAACCCCAAGATCCAGGTTTTCGAGACTCTGAGGTCTCGAGGCGCTAC 1065
Qy 221 GlyGlyAlaAsnGlyProLeuAlaGlyValIleValLysAsnLeuLeuAsnGlyGlu 240
Db 1066 GCGCGCGAGGTGAGGTCCATTGGCTGGTGTCAAGGTGAAGACTTGGTACTGGGAAG 1125
Qy 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
Db 1126 ATCTCCGACCTTCAGGTCTCGGTCTCTTCTTCGACATCGACATGAACCGGACGAG 1185
Qy 261 PheLeuGlyGlyGlnLeuLeuAspSerAspGlyTyrValGluThrLysProGlySer 280

Db 1186 TTTCGCGCGGCGAGCTTCAGCTCGATGCTGATGGTATGTGGCCACCAAGCCAGGCTCC 1245
Qy 281 ThrHisThrSerValIleGlyValPheAlaAlaGlyAspValGlnAspLysTyrArg 300
Db 1246 ACCACACACAGTGTGAAGGGGCTTTTGTCTGGGATGTGCAGGACCAAGATATCGC 1305
Qy 301 GlnAlaIleThrAlaAlaGlySerGly 309
Db 1306 CAGGCTATTACTGCGCGCTGATCAGGT 1332

RESULT 3
ADA70761
ID ADA70761 standard; DNA; 1130 BP.

XX ADA70761;

DT 20-NOV-2003 (first entry)

XX Rice gene, SEQ ID 4084.

XX Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.

XX Oryza sativa.

XX WO2003000898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
DR WPI; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.

XX Claim 6; SEQ ID NO 4084; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

XX Sequence 1130 BP; 174 A; 419 C; 358 G; 179 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,75e-136 Length: 1130
Score: 1409.00 Matches: 269
Percent Similarity: 94.81% Conservative: 23
Best Local Similarity: 87.34% Mismatches: 16
Query Match: 82.45% Indels: 0
DB: 7 Gaps: 0

US-10-005-429-25 (1-331) x ADA70761 (1-1130)

Qy 1 MetGluGlySerAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20

Db 112 ATGAGGAGCGGCGCGCGCGCTGCGCGCGGTGTGTCATCATCGGAGCGGCGG 171

DR P-PSDB; AAB29250.
 XX Recombinant or isolated nucleic acid, useful for producing transgenic
 PT plants with altered redox properties, encode thioredoxin h or thioredoxin
 PT reductase.
 XX
 XX Claim 66; Fig 5B; 125pp; English.
 XX
 CC The present invention relates to the isolation and use of the barley
 CC thioredoxin h and NADPH-thioredoxin reductase coding and protein
 CC sequences. Thioredoxin is thought to be involved in plant development via
 CC its function in the reduction of disulfide bridges. Thioredoxin can be
 CC used in hair care products and in the neutralisation of some venoms and
 CC toxins, and is also useful in the reduction of some food, for example it
 CC can be used to reduce the allergenicity of foods and the digestibility of
 CC some proteins. It can also be used to enhance the baking qualities of
 CC cereal flour
 XX
 SQ Sequence 1991 BP; 338 A; 675 C; 591 G; 368 T; 0 U; 19 Other;
 Alignment Scores:
 Pred. No.: 9.54e-150 Length: 1991
 Score: 1542.00 Matches: 302
 Percent Similarity: 94.26% Conservative: 10
 Best Local Similarity: 91.24% Mismatches: 19
 Query Match: 90.23% Indels: 1
 DB: 3 Gaps: 0
 US-10-005-429-25 (1-331) x AAC62460 (1-1991)
 QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleGlySerGlyPro 20
 DB 1 ATGGAGGATCGCGGCGCGCGCGTCCGACGCGGCGTGCATCATCGGCGCGCGCG 60
 QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
 DB 61 GCGCGGCACACGCGCGCGCATCTACCGCGCGCGCGCGGAGCTCAAGCGGCTCTTCGAG 120
 QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
 DB 121 GCCTCGATGCGCCACGACATCGCGCGGCGCGCGAGCTCACACACCGACGCTCGAG 180
 QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
 DB 181 AACTTCCCGGATTCGCCCGCGCATCATGGCGCATCGACCTCATGACCAACTCGCGCGCC 240
 QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
 DB 241 CAGTCCGCTCCGCTTCGCGACCAACATCTCTCCGAGACCGTCCCGAGGTTCGACTTCTCC 300
 QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
 DB 301 GCCCGCCCTTCGGGTCACCTCCGACTCCACACCGCTCTCGCGGACANCGTCGCTGTC 360
 QY 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
 DB 361 GCCCGGGCGCGTCCGCGCGCGCTCCATTC -TCGGTTCGACACCTTACTTGGAAACGCG 419
 QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
 DB 420 GGCATCTCCGCTCGCGCGTCTCGGACGCGCGTCCGCGCCCATCTTCGGAACAAGCCCATC 479
 QY 161 AlaValIleGlyGlyCysSerAlaMetGluGluSerAsnPheLeuThrIleTyrGly 180
 DB 480 GCGGTTCATCGCGCGCGGTATTCGCGCATGCGAGGAGGCAACTTCTCTCAAGTACGGA 539
 QY 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
 DB 540 TCCCAAGTGTATCATCATCCGCGCGCAACACTTCGCGCGCTCCCAAGTATATGAGGCT 599
 QY 201 ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyr 220
 DB 600 AGGCGGCTCTCCAAATCCTTAAGATCCNGGTTGTCTGGACTCGGAGGTCTCGAGGCTTAC 659

QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
 DB 660 GCGCGTGCAGCGCGCGCCCATTTAGCTGGGGTCAAGGTCAAGAACTTGGTACTGGTGA 719
 QY 241 ValSerAspLeuGlnValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
 DB 720 GTGTCTGACCTTCAGGTGTCGGGCTTTCTTCGCCATCGGGCATGAGCCGCCACCAAG 779
 QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
 DB 780 TTCTCAATCGCGAGCTTGAAGTCCATGCGGATGGGTATGTGGCCACCAAGCCGGGTCT 839
 QY 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArg 300
 DB 840 ACACATACCAAGTGGAGGGGCTTTTGTGCTGGAGACGTGCACAGGATAGAAGTATCG 899
 QY 301 GlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeu 320
 DB 900 CAGGCCATTACTGCTGCTGCATCAGGTTGCATGCTGCTTTGGACGCCGAGCACTATCTG 959
 QY 321 GlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
 DB 960 CAGGAGTGGTGCACAGGTGGGCAAGTCTGAT 992
 RESULT 2
 AAD29838
 ID AAD29838 standard; DNA; 1560 BP.
 XX
 AC AAD29838;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Rice NADPH dependent thioredoxin reductase DNA (NTR).
 XX
 KW Transgenic plant; thioredoxin reductase; starch; protein; grain;
 KW milling process; enzyme; rice; ds.
 XX
 OS Oryza sativa.
 XX
 FH Key Location/Qualifiers
 FT CDS 406..1338
 FT /*tag= a
 FT /product= "Rice NTR"
 XX
 PN WO200198509-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 19-JUN-2001; 2001WO-EP006918.
 XX
 PR 21-JUN-2000; 2000US-00598747.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Lanahan MB, Desai NM, Gasdaaka PY;
 XX
 DR WPI; 2002-179557/23.
 DR P-PSDB; AAB18733.
 XX
 PT Transgenic plant coding for eukaryotic thioredoxin reductase at elevated
 PT levels useful for separating the starch and protein components of grain
 PT in a milling process.
 XX
 PS Claim 12; Page 81; 86pp; English.
 XX
 CC The present invention relates to a transgenic plant comprising
 CC heterologous DNA coding for eukaryotic thioredoxin reductase integrated
 CC into its nuclear or plastid genome and use of thioredoxin reductase for
 CC separating the starch and protein components of grain in a milling
 CC process. Transgenic plant is used for separating the starch and protein
 CC components of grain in a milling process. Transgenic plant may be used to
 CC produce thioredoxin reductase at elevated levels. Delivery of thioredoxin

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 5, 2004, 00:59:23 ; Search time 425.882 Seconds
(without alignments)
3301.746 Million cell updates/sec

Title: US-10-005-429-25

Perfect score: 1709

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Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-USER=US10005429 -CGN_1_1_886 -runat_04052004_121648_15427 -NCFU=6 -ICFU=3
-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 29Jan04:*

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2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1542	90.2	1991	3 AAC62460	Aac62460 Barley NA
2	1478	86.5	1560	6 AAD29838	Aad29838 Rice NADP
3	1409	82.4	1130	7 ADA70761	Ada70761 Rice gene
4	1365	79.9	963	7 ADA70332	Ada70332 Rice gene
5	1335.5	78.1	1152	3 AAC43307	Aac43307 Arabidops
6	1335.5	78.1	1152	6 ABZ14681	Abz14681 Arabidops
7	1335.5	78.1	1152	7 ADA67905	Ada67905 Arabidops
8	1335.5	78.1	1375	3 AAC48213	Aac48213 Arabidops

9	1318	77.1	1002	6 ABN89578	Abn89578 Arabidops
10	1318	77.1	1002	6 ABN89576	Abn89576 Arabidops
11	1318	77.1	1002	6 ABS53094	Abs53094 DNA encod
12	1318	77.1	1438	3 AAC38830	Aac38830 Arabidops
13	1318	77.1	1539	3 AAC36511	Aac36511 Arabidops
14	1318	77.1	3787	6 ABN89582	Abn89582 Phascolin
15	1318	77.1	3787	6 ABS53098	Abs53098 CDNA enco
16	1318	77.1	4545	6 ABN89584	Abn89584 Phascolin
17	1318	77.1	4545	6 ABS53100	Abs53100 DNA encod
18	1318	77.1	4546	6 ABN89583	Abn89583 Phascolin
19	1318	77.1	4546	6 ABS53099	Abs53099 DNA encod
20	1318	77.1	6357	7 AAL54488	Aal54488 Thioedox
21	1318	77.1	6357	7 AAL54492	Aal54492 Thioedox
22	1318	77.1	6357	9 ADD26530	Add26530 Thalecres
23	1318	77.1	6357	9 ADD26536	Add26536 Thalecres
24	1317	77.1	1540	3 AAC51123	Aac51123 Arabidops
25	1306	76.4	6357	7 AAL54485	Aal54485 Thioedox
26	1306	76.4	6357	9 ADD26523	Add26523 Thalecres
27	1306	76.4	6357	9 ADD26533	Add26533 Thalecres
28	1305	76.4	6357	7 AAL54487	Aal54487 Thioedox
29	1305	76.4	6357	9 ADD26525	Add26525 Thalecres
30	1304	76.3	6357	7 AAL54494	Aal54494 Thioedox
31	1304	76.3	6357	7 AAL54484	Aal54484 Thioedox
32	1304	76.3	6357	9 AAL54490	Aal54490 Thioedox
33	1304	76.3	6357	9 ADD26528	Add26528 Thalecres
34	1304	76.3	6357	9 ADD26522	Add26522 Thalecres
35	1304	76.3	6357	9 ADD26532	Add26532 Thalecres
36	1303	76.2	6357	7 AAL54493	Aal54493 Thioedox
37	1303	76.2	6357	9 ADD26531	Add26531 Thalecres
38	1303	76.2	6357	9 ADD26534	Add26534 Thalecres
39	1302	76.2	6357	9 ADD26524	Add26524 Thalecres
40	1302	76.2	6357	9 ADD26517	Add26517 Thalecres
41	1302	76.2	6408	7 AAL54482	Aal54482 Thioedox
42	1298	76.0	6306	7 AAL54479	Aal54479 Thioedox
43	1298	76.0	6356	9 ADD26529	Add26529 Thalecres
44	1298	76.0	6357	7 AAL54491	Aal54491 Thioedox
45	1298	76.0	6357	9 ADD26520	Add26520 Thalecres

ALIGNMENTS

RESULT 1

AAC62460

ID AAC62460 standard; DNA; 1991 BP.

XX AAC62460;

XX AC AAC62460;

XX DT 07-FEB-2001 (first entry)

XX DE Barley NADPH-thioedoxin reductase coding sequence.

XX KW Barley; NADPH-thioedoxin reductase; disulfide bridge reduction; NTR;

KW development; thioedoxin h; hair care product; venom neutralisation;

KW food technology; food allergy; ds.

XX OS Hordeum vulgare.

XX PN WO200058352-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US008556.

XX PR 31-MAR-1999; 99US-0127198P.

XX PR 06-DEC-1999; 99US-0169162P.

PR 21-JAN-2000; 2000US-0177739P.

PR 21-JAN-2000; 2000US-0177740P.

XX (REGC) UNIV CALIFORNIA.

PI Cho M, Del Val G, Caillaud M, Lemaux PG, Buchanan BP;

XX WPI; 2000-679291/66.


```

Qy 79 ArgAlaGlnSerLeuArgPheGlyThrAenIleLeuSerGluThrValThrAlaValAsp 98
Db 65537 AGAAAACAATCGAGAGATTGGAACTACGACTCTTCAAGAACTGTTAAACAAAGTTGAT 65596
Qy 99 PheSerAlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
Db 65597 TTCTCATCGAAACCGTTTAAGCTATTCTACTGATTGAGAACGTTTCTGCTGATTTCTGTA 65656
Qy 119 IleValAlaThrGlyAlaValAlaAlaArgLeuHisPheProGlySer----- 134
Db 65657 ATCATTTCTACTGGAGCTGTGCTAAACGCTTAGCTTCACTGGATCTGGTGAAGGTAAT 65716
Qy 135 AspAlaTyrTTPAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
Db 65717 GGTGGTTTTTGGAAATCGTGATATCCCGCTTGTCTGTGTTTGGACGGAGCTCTCCGATT 65776
Qy 155 PheArgAsnLysProIleAlaValIleGlyGlyGlyAspSerAlaMetGluGluSerAsn 174
Db 65777 TTTAGGAATAAGCCTCTTGCTGTTATTTGGTGTGTTGATTTAGCTATGGAGGAGCGAAT 65836
Qy 175 PheLeuThrLysTyrGlySerHisValTyrIleIleHisArgArgAsnThrPheArgAla 194
Db 65837 TTTCTGACTAAGTATGGAATCTAAGGTTTATATTATTCATAGGAGGATAOCTTTAGGGCG 65896
Qy 195 SerLysIleMetGlnAlaArgAlaLeuGluAsnProLysIleLysValIleuTrpAspSer 214
Db 65897 TCTAGATTATACAGCAGAGAGCTTTGCTAACCCCTAGATTGAGTGTGATTGGAACTCT 65956
Qy 215 GluValValGluAlaTyrGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLys 234
Db 65957 GCCGTGGTTGAGCGGTATGGTGATGAAATGGACGTTCTTTGGAGGATTGAAGGTGAAG 66016
Qy 235 AsnLeuLeuAsnGlyGluValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGly 254
Db 66017 AATGTTGTACTGGGATGTTTCAGATCTGAGAGGTGCTGGATTTCTTTGCTATTGGT 66076
Qy 255 HisGluProAlaThrLysPheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrVal 274
Db 66077 CATGAGCCAGCTACCGAAGTTTTTGGATGGCCAGCTTGAGCTTGATCAAGATGCTTATGTT 66136
Qy 275 GluThrLysProGlySerThrHisThrSerValLysGlyValPheAlaGlyAspVal 294
Db 66137 GTGACCAAGCCAGGACTACTAAGACGACGGTGGTGGTGTATTTGCTGCTGGAGATGTT 66196
Qy 295 GlnAspLysLysTyrArgGlnAlaIleThrAlaGlySerGlyCysMetAlaAlaLeu 314
Db 66197 CAAGACAAGAAGTATAGACAGGCCCATCACTGCTGCAGGAACGTGTTTGTACTCTTAACCTTG 66256
Qy 315 AspAlaGluHisTyr 319
Db 66257 TATTTTTTACATTTC 66271

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Search completed: May 5, 2004, 04:58:05
Job time : 4095.73 secs

Percent Similarity: 85.54% Conservative: 27
 Best Local Similarity: 77.23% Mismatches: 43
 Query Match: 75.48% Indels: 4
 DB: 6 Gaps: 1

US-10-005-429-25 (1-331) x AX366997 (1-1021)

Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyrAlaAla 30
 Db 34 ACCCGCTTCGATCGCTGGCTCGCGCGCTGCGCCACCGCGCCATTCAGCGGCC 93

Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50
 Db 94 CGCGCGAGCTGAGCGCGCTCTCTTCGAGGCTGATGGCAACAGCATCGCCCGGC 153

Qy 51 GlyGluLeuThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 70
 Db 154 GGCAGCTCACCACCAACCGACGCTGAGAACTTCGCGGCTTCGCGAGGATCTCTC 213

Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
 Db 214 GCGTGGCTGACCGACGAGTTCGACGAGGAGCGGCTTCGGCACCATCTTC 273

Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
 Db 274 ACCGAGACGCTGACCAAGTGCGATCTTCGAGAGCGGCTTCAGGCTCTTCACCGACTCC 333

Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArgLeuHis 130
 Db 334 AAGGCCATCTCGCGACGCGGATCTTCGCGCATCGCGCGCGTGGCGAAGTGGCTCTCC 393

Qy 131 PheProGlySer-----AspAlaTyrTrpAsnArgGlyIleSerAlaCysAla 146
 Db 394 TTCGTGGCTCGCGGAGGTGCTCGCGGCTCTGCAACCGCGCATCTCGCGCTCGGCT 453

Qy 147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
 Db 454 GTGTGGAGCGCGCGCGCGCTCTTCGCAACAGCGCGCTCGCTGTGATCGTGGCGGA 513

Qy 167 AspSerAlaMetGluSerAsnPheLeuThrLysTyrGlySerHisValTyrIleIle 186
 Db 514 GACAGCGGATGGAGGAGCGGCGGCTCTTCACCAAGTACGCTCCAGGTGTATCATCTC 573

Qy 187 HisArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
 Db 574 GACCGCGGACGCGCTTCGCGGCTCCAAGATCATGACGAGCGCGGCTCTCCAAACCG 633

Qy 207 LysIleLysValLeuThrPheSerGluValValGluAlaTyrGlyGlyAlaAsnGlyGly 226
 Db 634 AAGATGAGCTGATGAGAGCTCTCCGCGTGGAGGCTACGCGGAGCGCGCGCGGAC 693

Qy 227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
 Db 694 GTGCTCGCGGCTCAAGGTGAAGACGTTGTCGCGGCGGCTCTCCGACCTCAAGGTG 753

Qy 247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlyGly 266
 Db 754 TCGCGGCTCTCTTCGCGCATCGCGGCTGACGCGCGGCGGCGGCTCTTCGCGCGGCGGT 813

Qy 267 GluLeuAspSerAspGlyTyrValGluThrLysProGlySerThrHisThrSerValLys 286
 Db 814 GAGCTGAGCTCCGAGCGCTACGCTGCTGACCAAGCGCGGCGGCGGCGGCTCTCGTGCCT 873

Qy 287 GlyValPheAlaAlaGlyAspValGlnAspLysLysTyrArgGlnAlaIleThrAlaAla 306
 Db 874 GCGGTGTTCGCGCGCGCGCGCTGAGGAGCAAGAGTACCGCGAGGCTCACCGCGCGCC 933

Qy 307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrLeuGlnGluIleGlyAlaGln 326
 Db 934 GGCACCGGCTGATGCGCGCGCTTCGACGCGCGGAGCACTACCTCCAGAGATCGGCTCCGAG 993

Qy 327 GlyGlyLysSerAsp 331

994 GAGGCGAGTCCGAC 1008

Db

RESULT 14

ATTHREDB

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PubMed

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

Location/Qualifiers

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/tissue_type="silique"

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96. .1094

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/protein_id="CAA80656.1"

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 LFTSGKALADAVILAI GAVAKWLSFVSGEVLGLWNRGISACVCDGAAPIFRNP
 LAVIGGSADAMEANFLTKYGSKVYIDRDAFRANMOQRALSNPKIDVWNSVYV
 EAYGGERDLVGLKVNVTGSDVSLKVSGLFPAIGHEPATKFLDGGVELDSGYV
 TKFGTQTSVPGVAFAGVDQKKYRQALTAAGTCGMAALDAEHVLQSIGSQGKSD"

Alignment Scores:

Pred. No.: 9,86e-96 Length: 1261

Score: 1244.50 Matches: 245

Percent Similarity: 83.69% Conservative: 27

Best Local Similarity: 75.38% Mismatches: 5

Query Match: 72.82% Indels: 48

DB: 8 Gaps: 2

US-10-005-429-25 (1-331) x ATTHREDB (1-1261)

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Db 120 ACAAGCTCTGATGAGGAGTGGCCGCGGACACACGCGCGGCGATTCGCGAGCT 179

Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTyrMetAlaAsnAspIleAlaAlaGly 50

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submitted to Genbank.
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                        /db_xref="taxon:3702"
                        /chromosome="4"
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                        /ecotype="Columbia"
                        /note="This clone is in a modified pBluescript vector2
                        (lambda PS) as a BamHI/XhoI insert."
     gene              1..1433
                        /gene="At4g35460"
     5'UTR             1..73
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                        74..1075
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                        /protein_id="AAO42318.1"
                        /db_xref="GI:28393813"
                        /translation="MNGLETHNRLICIVGSPAAHTAAIYAARAELEKLLPEGMAND
                        IAPGGUTTTVDENPGFPEGILGVELTDKPKOSRPGTTFIETVTKVDSSKEF
                        KLFTDSXAILADAVLATGAVAKLSFVSGENGSGFWMRGISACVDCGAAPIFRNK
                        PLVIGGDSAMEANLTKYGSVYIIHRDAFRASKIMQORALSVPKIDVFNWSSV
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Percent Similarity: 86.46%           Conservative:    27
Best Local Similarity: 78.15%         Mismatches:      40
Query Match:       76.95%             Indels:          4
DB:                8                  Gaps:            1

US-10-005-429-25 (1-331) x EF004322 (1-1433)
Qy 11 ThrArgIleCysIleIleGlySerGlyProAlaAlaHisThrAlaAlaIleTyzAlaAla 30
Db 98 ACAGGCTCTGTATGTAGGAGTGGCCAGCGGCACACACGCGCGGATTTACGCAGCT 157
Qy 31 ArgAlaGluLeuLysProValLeuPheGluGlyTrpMetAlaAsnAspIleAlaGly 50
Db 158 AGGGCTGAACCTTAACTCTCTCTCTGGAAGATGATGGTAAACGATCGCTCCCGGT 217
Qy 51 GlyGlnLeuThrThrThrAspValGluAsnPheProGlyPheProAsnGlyIleMet 70
Db 218 GGTCAACTAAACACACCCAGCGTCCGGAATTTCCCGGATTTCCAGAGGATTTCTC 277
Qy 71 GlyAlaAspLeuMetAspAsnCysArgAlaGlnSerLeuArgPheGlyThrAsnIleLeu 90
Db 278 GGAGTAGAGCTCACTGACAAATTCGTAAACATCGAGCGATTCGGTACTACGATATT 337
Qy 91 SerGluThrValThrAlaValAspPheSerAlaCysProPheArgValSerAlaAspSer 110
Db 338 ACAGAGACGGTGACCAAGTGTGATTTCTTCGAAACCGTTTACGCTATTACAGATTCA 397
Qy 111 ThrThrValLeuAlaAspAlaValIleValAlaThrGlyAlaValAlaArgArgLeuHis 130

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398 AAGGCCATTCTCGCTGACGCTGTGATTCTCGCTACTGGAGCTGTGGCTAAGCGCTTAGC 457
131 PheProGly-----SerAspAlaIleTyzTrpAsnArgGlyIleSerAlaCysAla 146
458 TTCGTTGGATCTGGTGAAGCTTCTGGAGGTTTCTGGAAACGCTGGAATCTCCGCTTGCT 517
147 ValCysAspGlyAlaAlaProIlePheArgAsnLysProIleAlaValIleGlyGly 166
518 GTTTCGACGAGCTGCTCCGATATTCCGTAACAAACCTCTTCGGGTGATCGGTGAGGC 577
167 AspSerAlaMetGluGluSerAsnPheLeuThrLysTyzGlySerHisValTyzIle 186
578 GATTTCAGCAATGGAGAGCAACTTCTTACAAATATGGAATCTAAAGTGTATATAATC 637
187 HisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAlaLeuGluAsnPro 206
638 CATAGAGAGATGCTTTTAGAGCGTCTAAGATTATGACGAGCGAGCTTTGTCTAATCCT 697
207 LysIleLysValLeuTrpAspSerGluValValGluAlaTyzGlyGlyAlaAsnGly 226
598 AAGATTGATGTTGTTTGGAACTGCTGTTGTGGAAGCTTATGGAGATGGAGAAAGAT 757
227 ProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGluValSerAspLeuGlnVal 246
758 GTGCTTGGAGGATTGAAGTGAAGAATGTGCTTACCGGAGATGTTTCTGATTTAAAGTT 817
247 SerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeuGlyGlnLeu 266
818 TCTGGATGTTCTTGTATGTTGTCATGTCAGCCAGCTACCAAGTTTTCGATGTTGTT 877
267 GluLeuAspSerAspGlyTyzValGluThrLysProGlySerThrHisThrSerValLys 286
878 GAGTAGATTCCGATGCTTATGTTGTCCAGAGCTGGTACTACACAGACTAGCGTTCCC 937
287 GlyValPheAlaAlaGlyAspValGlnAspLysTyzArgGlnAlaIleThrAlaAla 306
938 GAGATTTTTCCTCGCGGTGATGTTTCAGGATAAGATATAGGCAAGCCATCCTCTGCA 997
307 GlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyzLeuGlnGluIleGlyAlaGln 326
998 GGAAGTGGTGCATGGCGCTTTGGATGCAGAGCATTACTTACAGAGATTGGATCTCAG 1057
327 GluGlyLysSerAsp 331
1058 CAAGTAAGAGTGTAT 1072

RESULT 13
AX366997 1021 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 24 from Patent WO0198509.
ACCESSION AX366997
VERSION AX366997.1 GI:18698274
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE
 1 Lanahan,M.B., Desai,N.M. and Gasdaska,P.Y.
  Grain processing method and transgenic plants useful therein
  Patent: WO 0198509-A 24 27-DEC-2001;
  Syngenta Participations AG (CH)
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ORIGIN
Alignment Scores:
Pred. No.:          1.1e-99          Length:          1021
Score:             1290.00           Matches:         251

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS
Chang H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Qian, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.

TITLE
JOURNAL
Plant genes involved in defense against pathogens
Patent: WO 0300898-A 148 03-JAN-2003;
Syngenta Participations AG (CH)

FEATURES
source
1. 1152
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

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Alignment Scores:
Pred. No.: 1.85e-103 Length: 1152
Score: 1335.50 Matches: 258
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Best Local Similarity: 76.56% Mismatches: 36
Query Match: 78.15% Indels: 9
DB: 6 Gaps: 2

US-10-005-429-25 (1-331) x AX651358 (1-1152)

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QY 19 GlyProAlaAlaHisThrAlaAlaIleTyAlaAlaArgAlaGluLeuLysProValLeu 38
DB 199 GGCACGACGACACACGCGCGCGATCATCGATCGAGCGGAGCTTAAGCCCTCTCTC 258

QY 39 PheGluGlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAsp 58
DB 259 TTCAGAGATGGATGGGTACGACGATCGCTCCCGCGGTCAATTAATACAAACCGAC 318

QY 59 ValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCys 78
DB 319 GTCGAAATCTCCCTGGTTCCTCGAGGATTCCTCGTATTGATATCGTTGAGAAATTC 378

QY 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAsp 98
DB 379 AGAAACAAATCGGAGATTTGGAACTACGATCTTCACGAAACTGTTAAACAAAGTTGAT 438

QY 99 PheSerAlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
DB 439 TTCTCATCGAAACCGTTTAACTTATTCACCTGATTCGAGAACTGTTCTCGCTGATTCGTA 498

QY 119 IleValAlaThrGlyAlaValAlaAlaArgArgLeuHisPheProGlySer----- 134
DB 499 ATCATTTCTACTGAGCTGTGCTAAACGCTTACGCTTCATCGATCTGGTGAAGGTAAT 558

QY 135 AspAlaTyTrpAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
DB 559 GGTGGTTTGGATCGGTGATCTCGCTTGTGCTTTGGACGAGGCTGCTCGATT 618

QY 155 PheArgAsnLysProIleAlaValIleGlyGlyCysSerAlaMetGluGluSerAsn 174
DB 619 TTTAGGAATAAGCCTCTGTGGTTATTGGTGGTGGTGAATTCAGCTATGGAGGAAGCAAT 678

QY 175 PheLeuThrLysTrpGlySerHisValTyIleIleHisArgArgAsnThrPheArgAla 194
DB 679 TTTCTGACTAAGTATGATCTAAGGTTTATATTATTCATAGGAGGATGATGTTTAGGCG 738

QY 195 SerLysIleMetGlnAlaAlaGlnAlaLeuGluAsnProLysIleLysValLeuTrpAspSer 214
DB 739 TCTAAGATTATCGACGACAGAGCTTTGTCCTAACCCCTAAGATTGAAGTATTCGAACTCT 798

QY 215 GluValValGluAlaTyGlyAlaAsnGlyCysProLeuAlaGlyValLysValLys 234
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QY 235 AsnLeuLeuAsnGlyGluValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGly 254
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QY 255 HisGluProAlaThrLysPheLeuGlyGlnLeuGluLeuAspSerAspGlyTrpVal 274
DB 919 CATGAGCCAGCTACGAAGTTTTCGATGGGACCTTGAGCTTGTGAAGATGTTTATGTT 978

QY 275 GluThrLysProGlySerThrHisThrSerValLysGlyValPheAlaAlaGlyAspVal 294
DB 979 GTGACCAAGCCAGCTACTACTAAGACGAGCGGTGTTGGTGTATTTGCTGCTGGAGATGTT 1038

QY 295 GluAspLysLysTyArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu 314
DB 1039 CAAGACAAGAAATATAGACAGGCGCATCTGTCGAGGAACCTGGGTGTCATGGCGGCATTG 1098

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RESULT 12
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LOCUS
DEFINITION
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Arabidopsis thaliana clone RAF116-02-L06 (R50174) putative
thioredoxin reductase (NADPH) 2 (At4g35460) mRNA, complete cds.

ACCESSION
BT004322.1 GI:283939818
VERSION
FLI CDNA.
KEYWORDS
Arabidopsis thaliana (thale cress)
SOURCE
ORGANISM
Arabidopsis thaliana
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1 (bases 1 to 1433)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,
Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M.,
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,
Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W.,
Ecker, J.R. and Theologis, A.
Arabidopsis Full Length cDNA Clones
Unpublished
2 (bases 1 to 1433)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,
Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M.,
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,
Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W.,
Ecker, J.R. and Theologis, A.
Direct Submission

TITLE
JOURNAL
REFERENCE
AUTHORS
Submitted (14-FEB-2003) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAPL cDNAs (RAPL cDNA: "RIKEN
Arabidopsis Full-length cDNA"): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

TITLE
JOURNAL
COMMENT
The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAPL cDNAs: Yamada, K., Chan, M.M.,
Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S.,
Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G.,
Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M.,
Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W.,
Ecker, J.R. and Theologis, A.
Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC)
contributed equally to this work as PIs.
Annotation based on July 2002 version of the Arabidopsis genome

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Qy 161 AlaValIleGlyGlyGlyAspSerAlaMetGluSerAsnPheLeuThrLysTyrGly 180
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Db 601 AGGCGTGTGTCAACCCCAAGATCCAGGTTTCTGGGACTCTGAGGTCTGCGAGCCCTAC 660
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Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 700 -----GTTCTCGTCTCTTCTTCGCCATCGGCATGATCAACCGGCGACGAAG 744
Qy 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
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Qy 281 ThrHisThrSerValLysGlyValPheAlaIleGlyValAspValGlnAspLysLysTyrArg 300
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Db 865 CAGGCTATTACTCGCGCTGGATCAGATCAGTTCGCTTCATGCGGTTCG 912

RESULT 10
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LOCUS
DEFINITION Sequence 2486 from Patent WO0216655.
ACCESSION AX507791
VERSION AX507791.1 GI:23389028
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
1
REFERENCE
AUTHORS Harper, J.F., Krops, J., Wang, X. and Zhu, T.
TITLE Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL Patent: WO 0216655-A 2486 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
FEATURES
source
Location/Qualifiers
1..1152
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ORIGIN
Alignment Scores:
Pred. No.: 1,85e-103 Length: 1152
Score: 1335.50 Matches: 258
Percent Similarity: 86.85% Conservative: 34
Best Local Similarity: 76.56% Mismatches: 36
Query Match: 78.15% Indels: 9
DB: 6 Gaps: 2

US-10-005-429-25 (1-331) x AX507791 (1-1152)
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Db 139 TCCGCGCGCGCGCGCGCGATCGATCGAAGAACTCACAAACCAAGGTTTCATGCTCGGAAGT 198
Qy 19 GlyProAlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeu 38

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Db 259 TTCGAAGGATGATGCTAACACATCGTCCCGCGGCTCAATTAACTACACACACGAC 318
Qy 59 ValGluAsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspCys 78
Db 319 GTCGAAAACCTTCCTCGGTTCCCTGAAGGTATTCTCGGTATTGATATCGTTGAGAAATTC 378
Qy 79 ArgAlaGlnSerLeuArgPheGlyThrAsnIleLeuSerGlnThrValThrAlaValAsp 98
Db 379 AGAAACATTCGAGAGATTTGAACTACGATCTTCACGGAACCTGTTTAAACAAGTTGAT 438
Qy 99 PheSerAlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaVal 118
Db 439 TTTCTATCGAACAACCGTTTAAGCTATTCACTGATTCGAGAACTGTTCTCGCTGATCTGTA 498
Qy 119 IleValAlaThrGlyAlaValAlaAlaArgArgLeuHisPheProGlySer----- 134
Db 499 ATCATTTCTACTGAGAGCTGTTGCTAAACGCTTTAGCTTCCTGGAATCTGGTGAAGTAAT 558
Qy 135 AspAlaTyrTyrAsnArgGlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIle 154
Db 559 GGTGGTTTTTGGATCGTGTATCTCGCTGTGCTGTTTGGACGAGGCTGCTCCGATT 618
Qy 155 PheArgAsnLysProIleAlaValIleGlyGlyAspSerAlaMetGluGluSerAsn 174
Db 619 TTTAGGAATAAGCCTCTTGTGGTTATTGTGGTGGTGGTATTCAGCTATGAGGAAAGCGAAT 678
Qy 175 PheLeuThrLysTyrGlySerHisValTyrIleIleHisArgArgAsnThrPheArgAla 194
Db 679 TTTCTGACTAAGTATGATCTAAGGTTTATATTATTCATAGGAGGATACGTTTAGGGCG 738
Qy 195 SerLysIleMetGlnAlaArgAlaLeuGluAsnProLysIleLysValLeuThrAspSer 214
Db 739 TCTAAGATATTGCAGCAGAGAGCTTTGTCTCTAAGCTCTGAAGGTGCTCGATTGCTATTGGT 798
Qy 215 GluValValGluAlaTyrGlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLys 234
Db 799 GCGTGGTTGAGCGGATGATGATGAATGAGCGTGTCTTCGAGGATGAGGTTGAG 858
Qy 235 AsnLeuLeuAsnGlyGluValSerAspLeuGlnValSerGlyLeuPheAlaIleGly 254
Db 859 AATGTTGTTACTCGGATGTTTCAGATCTGAAGGTGCTCGATTGCTTCTTGTCTATTGGT 918
Qy 255 HisGluProAlaThrLysPheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrVal 274
Db 919 CATGAGCCAGCTACGAAGTTTTTGGATGGCGAGCTTGAGCTTGATGAAGATGTTATGTT 978
Qy 275 GluThrLysProGlySerThrHisThrSerValLysGlyValPheAlaAlaGlyAspVal 294
Db 979 GTGACCAAGCCAGGTACTACTAAGACGAGCGGTGGTGGTGTATTCTGCTGGAGATGTT 1038
Qy 295 GlnAspLysIleTyrArgGlnAlaIleThrAlaAlaGlySerGlyCysMetAlaAlaLeu 314
Db 1039 CAAGCAAGAAGTATAGACAGGCCCATCTGCTGCGAGGAAGTGGGTGCGATGCGCGCATG 1098
Qy 315 AspAlaGluHisTyrLeuGlnGluIleGlyAlaGlnGluGlyLysSerAsp 331
Db 1099 GATGCGAGCATTACTTACAGAGATTGATCTCAGAGGGGTAAAGATGAT 1149

RESULT 11
AX651358
LOCUS
DEFINITION Sequence 148 from Patent WO0300898.
ACCESSION AX651358
VERSION AX651358.1 GI:29154176
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"

ORIGIN

Alignment Scores:

Pred. No.: 1.13e-109 Length: 1130
Score: 1409.00 Matches: 269
Percent Similarity: 94.81% Conservative: 23
Best Local Similarity: 87.34% Mismatches: 16
Query Match: 82.45% Indels: 0
DB: 6 Gaps: 0

US-10-005-429-25 (1-331) x AX654214 (1-1130)

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QY 1 MetGluGlySerAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
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Db 112 ATGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 171

QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 172 GCGGCGCACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231

QY 41 GlyTyrMetAlaAlaHisThrAlaAlaGlyGlyGlnLeuThrThrThrThrThrThrThr 60
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 232 GCGTTCCTCCGCAACGACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 291

QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyValaAspLeuMetAspAsnCysArgAla 80
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 292 AACTTCCCGGGCTTCCCGAGCGCATCTCGCGCGCGCGCGCGCGCGCGCGCGCG 351

QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValaAspPheSer 100
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 352 CAGTCGTCGCGTTCGCGGACGAGATCTCACCAGAGACGCTCACCAGCGCTCGCTCG 411

QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 412 TCCCGCCCTTCGCGTCCGCTCCGCGCACCGCTGTCGACGCGCGCGCGCGCGCG 471

QY 121 AlaThrGlyAlaValaAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 472 GCACGCGCGCGCTCGCGCGCGCGCTCCATTTGCGCGGCTCCGACGATTCGGAACG 531

QY 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheAsnLysProIle 160
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 532 GGCATCTCCGCTGCGCGCTCTGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 591

QY 161 AlaValIleGlyGlyAspSerAlaMetGluGluSerAsnPheLeuThrLysTyrGly 180
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Db 592 GCGTTCGTCGCGCGCGGACTCCGCCATGAGAGAGGCCAACTTCTCACCAGTACG 651

QY 181 SerHisValTyrIleIleHisArgArgAsnThrPheArgAlaSerIleIleMetGlnAla 200
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 652 TCCCGCGTCTACATCATCCACCGCGCGCAACGCGCTTCGCGCGCTCCAGATCAT 711

QY 201 ArgAlaLeuGluAsnProLysIleLysValLeuTyrPheSerGluValValGluAlaTyr 220
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Db 712 CGGGCGCTCTCCACCCCAAGATCCAGTCTGCTGGACTCCGAGGTCTCGAGCGGTAC 771

QY 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuAsnGlyGlu 240
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 772 GCGCGCGCGAGCGCGGTTCGTTGGCGCGGCTCAAGGTCAAGGTCAAGGTGAGCGG 831

QY 241 ValSerAspLeuGluValSerGlyLeuPheAlaIleGlyHisGluProAlaThrLys 260
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 832 GTCTCCGACCTCCAGTTCGCGGGCTCTCTTCGCCATGTGGACGACGCGCGCAAG 891

QY 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyrValGluThrLysProGlySer 280
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 892 TTCTCCGCGGCGAGCTCGAGCTGAGCTCCGATGCTATGCTGACCAAGCGCGCTCC 951

QY 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGluAspLysTyrArg 300
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Db 952 ACTCACACAGCGTCAAGGAGTCTTCGCGCGCGGTGATGTTTCAGACAGAGATATCG 1011
QY 301 GlnAlaIleThrAlaAlaGlySer 308
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Db 1012 CAGGCCATTACTGCGCGCGGATCA 1035

RESULT 9
AX653785 963 bp DNA linear PAT 22-MAR-2003
LOCUS AX653785
DEFINITION Sequence 3655 from Patent WO03000898.
ACCESSION AX653785
VERSION AX653785.1 GI:29156599
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1
REFERENCE
AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 03000898-A 3655 03-JAN-2003;
Syngenta Participations AG (CH)
FEATURES
Location/Qualifiers
source 1..963
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"

ORIGIN

Alignment Scores:
Pred. No.: 4.8e-106 Length: 963
Score: 1365.00 Matches: 269
Percent Similarity: 89.24% Conservative: 13
Best Local Similarity: 85.13% Mismatches: 16
Query Match: 79.87% Indels: 18
DB: 6 Gaps: 3

US-10-005-429-25 (1-331) x AX653785 (1-963)
QY 1 MetGluGlySerAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
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Db 1 ATGAGAGATCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60

QY 21 AlaAlaHisThrAlaAlaIleTyrAlaAlaArgAlaGluLeuLysProValLeuPheGlu 40
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 61 TCGGCGCACACGCGCGCGATCTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120

QY 41 GlyTyrMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrThrThrThrThr 60
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 121 GCGTGGCTCGCCACAGACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

QY 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 181 AACTTCCCGGGTTCGCGAGGAGTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240

QY 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValaAspPheSer 100
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 241 CAGTCCCTCCGCTTCGCGCACGACATCTCCGAGACCGTCAAGCGCGGTCTCTTCC 300

QY 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 301 GCGCGCGCTTCGCGTTCGCTCCGACTCCACACCGGTCTCGCGCGCGCGCGGTCT 360

QY 121 AlaThrGlyAlaValaAlaArgArgLeuHisPheProGlySerAspAlaTyrTrpAsnArg 140
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 361 GCCACGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420

QY 141 GlyIleSerAlaCysAlaValCysAspGlyValaAlaProIlePheArgAsnLysProIle 160
   |||...|||...|||...|||...|||...|||...|||...|||...|||...|||...
Db 421 GGCATCTCCGCTGCGCGCTCTGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

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Db 1246 ACGCACACCACTGTGARGGGGCTTTCTGCTGGGATGTGCAGACAGAGTATCGC 1305
Qy 301 GlnAlaIleThrAlaAlaGlySerGly 309
Db 1306 CAGGCTATTACTGCGCTGGATCAGGT 1332

RESULT 7
AP005477
LOCUS AP005477 131980 bp DNA linear HTG 28-JUN-2002
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 6 clone
OSJNB0039F24, ** SEQUENCING IN PROGRESS ***
ACCESSION AP005477
VERSION AP005477.1 GI:21624397
KEYWORDS HTG; HTGS PHASE2.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
AUTHORS Sasaki, T., Matsumoto, T. and Katayose, Y.
TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
clone OSJNB0039F24
JOURNAL Published Only in Database (2002)
REFERENCE 2 (bases 1 to 131980)
AUTHORS Sasaki, T., Matsumoto, T. and Katayose, Y.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasakia@nias.affrc.go.jp, URL: http://rpg.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
COMMENT NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be replaced.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
Location/Qualifiers
1..131980
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="6"
/clone="OSJNB0039F24"

ORIGIN
Alignment Scores:
Pred. No.: 1,04e-107 Length: 131980
Score: 1416.00 Matches: 270
Percent Similarity: 94.53% Conservative: 24
Best Local Similarity: 86.82% Mismatches: 17
Query Match: 82.86% Indels: 0
DB: 2 Gaps: 0

US-10-005-429-25 (1-331) x AP005477 (1-131980)

Qy 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleGlySerGlyPro 20
Db 82633 ATGAGGAGGCGGCGCGGCGCGCTGCGGCGCGGTCATCATCGGAGCGGCGCG 82692

Qy 21 AlaAlaHisThrAlaAlaIleTyThrAlaAlaAlaAlaGluLeuLeuProValLeuPheGlu 40
Db 82693 GCGGCGCACACGCGCGCGCTACGCGCGCGCGCGAGCTCAAGCGCGTCTCTCGAG 82752

Qy 41 GlyTrpMetAlaAsnAspIleAlaGlyGlnLeuThrThrThrAspValGlu 60
Db 82753 GGCCTTCGCGCACGACGATCGCGCGCGGCGGCGAGCTCACACCACCGAGTCGAG 82812

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Qy 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
Db 82813 AACTTCCGGGCTTCCCGGACGCACTCTCGGCGCGACCTCATGACCGCTCCGCGCC 82872

Qy 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGlyThrValThrAlaValAspPheSer 100
Db 82873 CAGTCCGTGGCTTCGGGACCGAGATCTCACCGAGACCGTCACCGCGCTCGACCTCG 82932

Qy 101 AlaCysProPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db 82933 TCCGCGCCCTTCGCGCTCGCTCCGCGACACCGCTGTCACCGCGCGCTCGTGTG 82992

Qy 121 AlaThrGlyAlaValAlaArgArgLeuHisPheProGlySerAspAlaTyTrpAsnArg 140
Db 82993 GCCACGGGCGCGCTCGCGCGCGCTCCATTCGCGGCTCCGACGATTCGACCGCG 83052

Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaProIlePheArgAsnLysProIle 160
Db 83053 GGCATCTCCGCTCGCGCTGTCGACGCGCGCGCTCCATTCCTCCGGAACAAGCCATT 83112

Qy 161 AlaValIleGlyGlyValAspSerAlaMetGluGluSerAsnPheLeuThrLysTyGly 180
Db 83113 GCGTGTGTCGCGCGCGGAGCTCCGCACTGAGAGCGGCGGCTTCCTCACAAGTACGC 83172

Qy 181 SerHisValTyTrileIleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAla 200
Db 83173 TCCGCGCTCTACATCATCCACCGCGCGCTCCGCGCTCCAGATCATGACGCGC 83232

Qy 201 ArgAlaLeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyTr 220
Db 83233 CGGCGCTCTCCAAACCCCAAGATCCAGGTCTCTGGAGCTCCGAGGTCTCGAGGGGTAC 83292

Qy 221 GlyGlyAlaAsnGlyGlyProLeuAlaGlyValLysValLysAsnLeuLeuAsnGlyGlu 240
Db 83293 GCGCGCGCGCGCGCTCGTTCGTTGGCGGCGGTCAAGTCAAGTCAAGTCAAGTCAAG 83352

Qy 241 ValSerAspLeuGlnValSerGlyLeuPhePheAlaIleGlyHisGluProAlaThrLys 260
Db 83353 GTCTCCGACCTCCAGGTTCGCGCGCTCTTCTTCGCCATTGGACACGCGCGCGACAAAG 83412

Qy 261 PheLeuGlyGlyGlnLeuGluLeuAspSerAspGlyTyTrpValGluThrLysProGlySer 280
Db 83413 TTCTCGCGGCGCGCTCGAGCTGGAGTGGATGCTGTCGACCAAGCGCGCTCC 83472

Qy 281 ThrHisThrSerValLysGlyValPheAlaAlaGlyAspValGlnAspLysTyTrpArg 300
Db 83473 ACTCACACCGCTCAAGGAGTCTTCGCGCGCGGTGATGTTTCAGGACACAGAGTATCGC 83532

Qy 301 GlnAlaIleThrAlaAlaGlySerGlyCysMet 311
Db 83533 CAGGCGATTACTCGCGCGGATCAGGTACTA 83565

RESULT 8
AX654214
LOCUS AX654214 1130 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 4084 from Patent WO03000898.
ACCESSION AX654214
VERSION AX654214.1 GI:29157028
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 03000898-A 4084 03-JAN-2003;
Syngenta Participations AG (CH)
FEATURES source
Location/Qualifiers
1..1130

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Db 818 TTTCTCGCGGACAGCTCGAGCTCGACTCGAGGGGTACGTGGCCACCAAGCCGGGCTCC 87

[illegible]

Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Koijima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saichou,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shingawara,A., Shiraki,T., Sogabe,Y., Tagami,M., Tegami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
Location/Qualifiers
1..1383 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultiyar="Nipponbare" /db_xref="taxon:39947" /clone="#002-102-C03"
ORIGIN
Alignment Scores:
Pred. No.: 2,97e-118 Length: 1383
Score: 1512.00 Matches: 288
Percent Similarity: 94.53% Conservative: 23
Best Local Similarity: 87.54% Mismatches: 18
Query Match: 88.47% Indels: 0
DB: Gaps: 0
US-10-005-429-25 (1-331) x AKL06368 (1-1383)
Qy 3 GlySerAlaAlaProLeuArgThrArgGlyCysIlelleGlySerGlyProAlaAla 22
Db 170 GGAGGTCCCGGGCGCGCTGGCGGGCGCGGTGCATCATCGGAGGGGCCGGCG 229
Qy 23 HisThrAlaAlaIlePyrAlaAlaAroAlaGlueUlysProValLeuPheGluTrp 42
Db 230 CACACGGCGCGGCTTACCAGCGCGCGCGCGAGCTCAAGCCCGTGCTCTTCGAGGGCTTC 289
Qy 43 MetAlaAsnAspilealaalacgilyglinleuthrthrThrAspValgluAsnPhe 62
Db 290 CTCGCCAACGACATCGCGCGGGAGGCGAGCTCACCCACACCGAGCTCGAGAATTTC 349
Qy 63 ProGlyPheProAsnGlytIleMetGlyAlaAspleuMetAspAsnCysArgAlaGlnSer 82
Db 350 CGGGGCTCCCAGCGGACATCTCGCGCGCGACCTCATGGACCGCTGCGCGGCCACGTCC 409
Qy 83 LeuAtgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSerAlaCys 102
Db 410 GTGCGCTTCGGACACAGATCTCTCCAGAGACCTGCACCGCGCTCGACTCTCGTCCGC 469
Qy 103 ProPheArgValserAlaAspSerThrThrValLeuAlaAspAlaValileValAlaThr 122
Db 470 CCTTTCCGGCTCGCTCCCGGCACACCTCGTGACCGCGCGCGCGCTGCTGTCGCCACG 529
Qy 123 GlyAlaValAlaArxArgIleHisPheProGlySerAspAlaTyrrTroAsnAtgGlyIle 142
Db 530 GCGCGCTTCGGCGCGCGCTCCATTTCCCGCGCTCCGACGATCTCGAAACCGCGGATC 599
Qy 143 SerAlaCysAlaValCysAspGlyAlaAlaProillePheArgAsnLysProilleAlaVal 162
Db 590 TCCGCTCGCGCTCTGGACGGCGCGCGCCATCTTCOGGAACAAGCCCATTTGCCGTC 649
Qy 163 IleGlyGlyCysSerAlaMetGlnGluSerAsnPhelLeuThrLysTyrrGlySerHis 182
Db 650 GTTCGCGCGGGGATTCGCCCATGGAGAGGCCCAATCTTCCTCACCAAGTAGCGCTCCCGC 709
Qy 183 ValTyrrillelleHisArgArgAsnThrPheArgAlaSerLysIleMetGlnAlaArgAla 202
Db 710 GNTCATCATCATCCACCGCGCHACGCCCTTCGCGGGTCCAGATCATCGAGGCCCGCGGCC 769
Qy 203 LeuGluAsnProLysIleLysValLeuTrpAspSerGluValValGluAlaTyrrGlyGly 222
Db 770 CTCTCCACCCCAAGATCGCTCGTCTGGAGCTCCGAGCTCCGAGGTCGTCGAGGGGTACGGCGGC 829
b b

Qy	223	AlaAenGlyGlyProLeuAlaGlyVallysVallysAsnLeuLeuAenGlyGluValser	242
Db	830	GCGCAGCGCGGTCCGTTGGCGCGCTCAAGGTCAAGAACGTTGGTGCAGCGCGAGGTCTCC	889
Qy	243	AspLeuGlnValserGlyLeuPhePheAlaIleGlyHisGluProAlaThrLysPheLeu	262
Db	890	GACCTCCAGTCCCGCGCTCTTTTCGCCATTCGACACGACGCGCGACCAAGTTTTCTC	949
Qy	263	GlyGlyGlnLeuGluLeuAspSerAspGlyTyrrValGluThrLysProGlySerThrHis	282
Db	950	GCGCGGACGCTCGAGCTGGACTCGATGGCTATGTGTGTCGACCAAGCCCGGTCTCCAC	1009
Qy	283	ThrSerVallysGlyValPheAlaAlaGlyValAspValGlnAspLysTyrrArgGlnAla	302
Db	1010	ACCAGCGTCAAGGGAGTCTTTCGCCCGCGTGTATGTTTCAGGACCAAGAAGTATTCG	1069
Qy	303	IleThrAlaAlaGlySerGlyCysMetAlaAlaLeuAspAlaGluHisTyrrLeuGlnGlu	322
Db	1070	ATTACTGCCGCGGATCAGTTGCATGCGCGGTGTGATGTCGGAGCACTACTCTACAGG	1129
Qy	323	IleGlyAlaGlnGluGlySerAsp 331	
Db	1130	ATTGGAGCACAGACAGACAGACTGAT 1156	
RESULT 4	TAB421947		
LOCUS	TAB421947		
DEFINITION	Triticum aestivum mRNA for NADPH-thioredoxin reductase (ntf gene).		
ACCESSION	AJ421947		
VERSION	AJ421947.1 GI:17826832		
KEYWORDS	NADPH-thioredoxin reductase; ntf gene.		
SOURCE	Triticum aestivum (bread wheat)		
ORGANISM	Triticum aestivum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
TITLE	Poideae; Triticeae; Triticum.		
JOURNAL	Serrato,A.J.		
REFERENCE	B1 sistema tioredoxin h - tioredoxina reductasa de trigo.		
AUTHORS	Aislamiento y caracterizacion		
TITLE	Thesis (2002) Department of Biochemistry and Molecular Biology,		
JOURNAL	University of Sevilla, Sevilla, Spain		
REFERENCE	Serrato,A.J.		
AUTHORS	Cloning and functional characterisation of thioredoxin h reductase		
TITLE	From wheat		
JOURNAL	Unpublished		
AUTHORS	Cejudo,F.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-DEC-2001) Cejudo F.J., Inst. Bioquimica Vegetal y		
FEATURES	Fotosintesis, Universidad de Sevilla y CSIC, Avda Americo Vespucio		
source	s/n, 41092-Sevilla, SPAIN		
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	/db_xref="GOA:Q8VX47"		
	/db_xref="SPTREMBL:Q8VX47"		

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Qy 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaLeuLeuMetAspAsnCyArgAla 80
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RESULT 3
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LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:002-102-C03, full
            insert sequence.
ACCESSION AKI06368
VERSION AKI06368.1 GI:32991577
KEYWORDS FLI_CDNA; oligo capping.

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SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaroyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS

The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team;
Kikuchi S., Satoh K., Nagata T., Kawagashira N., Doi K.,
Kishimoto N., Yazaki J., Ishikawa M., Yamada H., Ooka H., Hotta I.,
Kojima K., Namiki T., Ohneda E., Iahagi M., Suzuki K., Li C.,
Ohtsuki K., Shishiki T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Ohtsuki K.,
Iida Y., Sugano S., Fujimura T., Suzuki Y., Tsunoda Y.,
Kurosaki T., Kodama T., Masuda H., Kobayashi M., Xie Q., Lu M.,
Narikawa R., Sugiyama A., Mizuno K., Yokomizo S., Miura J.,
Ikeda R., Ishibiki J., Kawanata M., Yoshimura A., RIKEN;
Kusumegi T., Oka M., Ryu R., Ueda M., Matsubara K., RIKEN;
Kawai J., Carninci P., Adachi J., Aizawa K., Arakawa T., Fukuda S.,
Hara A., Hashidume W., Hayatsu N., Imotani K., Ishii Y., Itoh M.,
Kagawa I., Kondo S., Konno H., Miyazaki A., Osato N., Ota Y.,
Saito R., Sasaki D., Sato K., Shibata K., Shinagawa A., Shiraki T.,
Yoshino M. and Hayashizaki Y.

TITLE

Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice

JOURNAL
MEDLINE

Science 301 (5631), 376-379 (2003)
22752273

PUBMED

12869764

REFERENCE

2 (bases 1 to 1381)

AUTHORS

Adachi J., Aizawa K., Akimura T., Arakawa T., Carninci P., Doi K.,
Fujimura T., Fukuda S., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayashizaki Y., Hayatsu N., Hiramoto K., Hiraoka T.,
Hori F., Hotta I., Iida Y., Ikeda R., Imamura K.,
Imotani K., Ishibiki J., Ishii Y., Ishikawa M., Itoh M., Kagawa I.,
Kikuchi S., Kishikawa Hirozane T., Kishimoto N., Kobayashi M.,
Kodama T., Kojima K., Kojima Y., Kondo S., Konno H., Kouda M.,
Koya S., Kurihara C., Kurosaki T., Kusumegi T., Li C., Lu M.,
Masuda H., Matsubara K., Matsuyama T., Miura J., Miyazaki A.,
Mizuno K., Murakami K., Murata M., Nagata T., Nakamura M.,
Namiki T., Narikawa R., Nishikura J., Nishi K., Nomura K.,
Numasaki R., Ohneda E., Ohno M., Ohtsuki K., Oka M., Ooka H.,
Osato N., Ota Y., Ohtsuki K., Ohtsuki K., Sakai C., Sakai K.,
Sakazume N., Sano H., Sasaki D., Sato K., Satoh K., Shibata K.,
Shinagawa A., Shiraki T., Shishiki T., Segabe Y., Sugano S.,
Sugiyama A., Suzuki K., Suzuki Y., Tagami M., Tagami-Takeda Y.,
Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka F., Tomaru A.,
Toya T., Tsunoda Y., Ueda M., Waki K., Xie Q., Yahagi W.,
Yamada H., Yamamoto M., Yasunishi A., Yazaki J., Yokomizo S. and
Yoshimura A.

TITLE

Direct Submission

JOURNAL

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305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,
Tel: 81-29-838-7007, Fax: 81-29-838-7007)

COMMENT

This clone is one of the 28K full-length cDNA clones from japonica
rice.

URL : <http://cdna1.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-Length cDNA Project Team: Kikuchi S., Satoh K.,
Nagata T., Kawagashira N., Doi K., Kishimoto N., Yazaki J.,
Ishikawa M., Yamada H., Ooka H., Hotta I., Kojima K., Namiki T.,
Ohneda E., Yahagi W., Suzuki K., Li C., Ohtsuki K., Shishiki T. and
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FAIS Genome Sequencing & Analysis Group: Ohtsuki K., Iida Y.,
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Kodama T., Kurosaki T., Kusumegi T., Lu M., Masuda H., Miura J.,
Mizuno K., Narikawa R., Nishikura J., Oka M., Ryo J., Sugano S.,
Sugiyama A., Suzuki Y., Tsunoda Y., Ueda M., Xie Q., Yokomizo S.,
Yoshimura A., Matsubara K. and Murakami K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi J., Aizawa K.,
Akimura T., Arakawa T., Carninci P., Fukuda S., Hanagaki T.,

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QY 181 SerHisValTyrIleHisArgAenThrPheArgAlaSerIlystleMetGlnAla 200
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RESULT 2
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DEFINITION insert sequence.
ACCESSION AK071251
VERSION AK071251.1 GI:32981274
KEYWORDS FLI CDNA; CAP trapper.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1
AUTHORS The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team;
Kikuchi,S., Satoh,K., Negata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Ohtsuki,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashizume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T.,
Yoshino,M., and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
JAPANESE 301 (5631), 376-379 (2003)
MEDLINE 22752273
PUBMED 12869764
REFERENCE 2 (bases 1 to 1502)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,

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Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kobayashi,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K.,
Nunakashi,R., Ohneda,E., Ohtsuki,K., Oka,M., Ooka,H.,
Osato,N., Ota,Y., Ohtsuki,Y., Ryu,R., Saitoh,H., Sakai,K.,
Sakazume,M., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
Shingawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,
Tagawa,A., Tanaka,T., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.
Direct Submission
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305-8602, Japan (E-mail:skikuchi@ias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
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URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
Negata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAJS Genome Sequencing & Analysis Group: Ohtsuki,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
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Genome Exploration Research Group in Riken Genomic Sciences Center
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Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Nunakashi,R., Ohno,M., Osato,N.,
Ota,Y., Saitoh,H., Sakai,K., Sasaki,D., Sato,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
Location/Qualifiers
FEATURES
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/clone="J023087H21"
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Score: 1590.00 Matches: 302
Percent Similarity: 96.37% Conservative: 17
Best local Similarity: 91.24% Mismatches: 12
Query Match: 93.04% Indels: 0
DB: 8 Gaps: 0
US-10-005-429-25 (1-331) x AK071251 (1-1502)
QY 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
Db 124 ATGGAGGGATCCGCGGGGCGCGCGCTCCGACGCGCGTGTGTCATCATCGGAGCGGCGCG 183

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AK104317
LOCUS AK104317 1389 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone.001-024-C03, full insert sequence.
ACCESSION AK104317
VERSION AK104317.1 GI:32989526
KEYWORDS FLI cDNA; oligo capping.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1
The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Xie, Q., Lu, M., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., International Science Genome Sequencing & Analysis Group: Ohtomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, M., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayaishizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)
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Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan E-mail: skkuchien@ias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007
This clone is one of the 28k full-length cDNA clones from japonica rice.
URL : <http://cdna01.dna.affrc.go.jp/cDNA/>
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FAIS Genome Sequencing & Analysis Group: Ohtomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Waki, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hangaki, F., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Kato, H., Kawai, J., Kishikawa-Hirozane, T., Kishimoto, N., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Oka, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayaishizaki, Y.
Location/Qualifiers
1. 1389
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="001-024-C03"

FEATURES
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1. 1389
9.22e-126 Length: 1389
1601.00 Matches: 303
Percent Similarity: 96.68% Conservative: 17
Best Local Similarity: 91.54% Mismatches: 11
Query Match: 93.68% Indels: 0
Gaps: 0

ORIGIN
Alignment Scores:
Pred. No.: 1389
Score: 1601.00
Percent Similarity: 96.68%
Best Local Similarity: 91.54%
Query Match: 93.68%
Indels: 0
Gaps: 0

US-10-005-429-25 (1-331) x AK104317 (1-1389)
Qy 1 MetGluGlySerAlaAlaAlaProLeuArgThrArgIleCysIleIleGlySerGlyPro 20
Db 108 ATGGAGGGATCCGGCGGGCGCGCGCTCCGACGCGCGTGTGCATCATCGGAGGGCGCG 167
Qy 21 AlalaHisThrAlaAlaIleTyAlaAlaArgAlaGluLeuTyProValLeuPheGlu 40
Db 168 TCGCGCGACACGCGGGGATCTACGCGCGCGCGCGGAGCTCAAGCCCGTCTTTCGAG 227
Qy 41 GlyTrpMetAlaAsnAspIleAlaAlaGlyGlyGlnLeuThrThrThrAspValGlu 60
Db 228 GCGTGGCTCGCCACAGACATCGCGCGGGGGCGCGCTCACACACCGCGCGTGGAG 287
Qy 61 AsnPheProGlyPheProAsnGlyIleMetGlyAlaAspLeuMetAspAsnCysArgAla 80
Db 288 AACTTCCCGGGTTCCCGCGAGGGGATCTCCGCGCGCGAGCTCATGGATCGCGCGGCC 347
Qy 81 GlnSerLeuArgPheGlyThrAsnIleLeuSerGluThrValThrAlaValAspPheSer 100
Db 348 CAGTCCCTCCCGTTCCGGCACCGCATCATCTCCGAGACCGCTCACCGCGGTGCGATTC 407
Qy 101 AlaCysPropPheArgValSerAlaAspSerThrThrValLeuAlaAspAlaValIleVal 120
Db 408 GCCTGCCCTTCCCGTCCCTCCGCTCCAGCTCCACACCGCTGCTCGCGCGCGTGTGTC 467
Qy 121 AlaThrGlyAlaValAlaAlaArgArgLeuHisPheProGlySerAspAlaTyTrpAsnArg 140
Db 468 GCCACCGCGCGCGTCCCGCGCGAGTCCACTTCGCCGGCTCCGAGCGCTACTGGAACGCG 527
Qy 141 GlyIleSerAlaCysAlaValCysAspGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 160
Db 528 GGCATCTCCGCTCGCGCGTCTGGAGCGGGCGCGCCCAATCTTCAGSAAACAAACCCATC 587
Qy 161 AlaValIleGlyGlyGlyAspSerAlaMetGluGlnSerAsnAspLeuThrThrIleTyGly 180
Db 588 GCCCTCATCGCGCGCGAGTCCGCCATGAGGAGTCCAACTTCTCTCCACCAAGTACGGC 647

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: May 5, 2004, 02:13:54 ; Search time 3993.73 Seconds
(without alignments)
3592.268 Million cell updates/sec

Title: US-10-005-429-25
Perfect score: 1709
Sequence: 1 MEGSAAPLRTRICIGSGP.....AALDAHYLQRIQAGEKSD 331

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xl
-O=/cp2 1/USPTO.spool.p/US10005429/runat 04052004 121649 15437/app query.fasta_1.782
-DB=GenEmbl -QPT=fastp -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10005429 @CCN 1 1 5417 @runat 04052004 121649 15437 -NCPG=6 -ICPU=3
-NO XMAP -LARGEQUERY -NEG SCORES=30 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
GenEmbl:.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.ph.*
24: em.pat.*
25: em.pl.*
26: em.ro.*
27: em.stb.*
28: em.un.*

29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.rod.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1601	93.7	1389	8	AK104317 Oryza sat
2	1590	93.0	1502	8	AK071251 Oryza sat
3	1512	88.5	1383	8	AK106368 Oryza sat
4	1510	88.4	1045	8	TA0421947 Trifolium
C 5	1479	86.5	118300	8	AP004165 Oryza sat
6	1478	86.5	1560	6	AX366999 Sequence
7	1416	82.9	131980	2	AP005477 Oryza sat
8	1409	82.4	1130	6	AX654214 Sequence
9	1365	79.9	963	6	AX653785 Sequence
10	1335.5	78.1	1152	6	AX507791 Sequence
11	1335.5	78.1	1152	6	AX651358 Sequence
12	1315	76.9	1433	8	BT004322 Arabidops
13	1290	75.5	1021	6	AX366997 Sequence
14	1244.5	72.8	1261	8	ATTHIREDB A.thaliana
15	1227.5	71.8	76170	8	AC002329 Arabidops
16	1219	71.3	1148	8	ATTHIREDA A.thaliana
17	1218.5	71.3	27408	8	AF1501 Arabidops
18	1218.5	71.3	197859	8	AY099756 Arabidops
19	1173	68.6	1128	8	U28372 Saccharomyc
20	1023	59.9	31184	8	BD021847 Thiorodox
21	1016	59.4	960	6	BD021847 Thiorodox
22	1011	59.2	963	6	AX488837 Sequence
23	1006	58.9	2592	8	U63713 Schizosacch
24	1006	58.9	3058	8	AF535134 Schizosacch
25	1006	58.9	17311	8	AL022019 S.pombe c
26	995	58.2	12130	1	AE011416 Leptospir
27	993.5	58.1	39954	8	YSC8263 Saccharomyc
28	985	57.6	2134	8	SCU10274 Saccharomyc
29	972.5	56.9	1000	8	AF532986 Pneumocys
30	972.5	56.9	1129	8	AF532987 Pneumocys
C 31	933.5	54.6	17004	1	AE001616 Chlamydia
32	933.5	54.6	23099	1	AE002205 Chlamydia
C 33	933.5	54.6	300380	1	AE017158 Chlamydia
C 34	933.5	54.6	300650	1	AP002546 Chlamydia
C 35	929.5	54.4	110000	6	AR310754_03 Continuation (4 of
36	922	53.9	2425	8	D45049 Neurospora
37	913.5	53.5	12426	1	AE001284 Chlamydia
38	908.5	53.2	300512	1	AE016995 Chlamydia
39	907.5	53.1	11147	1	AE002304 Chlamydia
40	905	53.0	1423	6	AR008096 Sequence
C 41	900	52.7	339650	1	AP003583 Nostoc sp
42	898	52.5	1572	8	AF541344 Pneumocys
43	897	52.5	1423	8	AF541344 Penicillium
C 44	894	52.3	298750	1	AP005375 Thermoosyn
45	877.5	51.3	5609	8	AY130996 Pneumocys

ALIGNMENTS

RESULT 1

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